

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 5, 2004, 15:54:17 ; Search time 60 Seconds
(without alignments)
1196.118 Million cell updates/sec

Title: US-09-895-814-525
Perfect score: 1369
Sequence: 1 MATAGNPMWFLGYLILGVA.....GVVTNLCKFTWEIKTVQAS 254

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1369	100.0	254	3	AAB21294 Human KLK
2	1369	100.0	254	4	AAM01174 Human pro
3	1369	100.0	254	4	Aau69819 Human pro
4	1369	100.0	254	4	AAG99059 Human pro
5	1369	100.0	254	4	ABU71710 Prostate
6	1369	100.0	254	5	ABb95279 Human P70
7	1369	100.0	254	6	ABP54360 Human KLK
8	1369	100.0	254	6	ABP54357 Human KLK
9	1369	100.0	254	6	ABR54391 Prostate
10	1369	100.0	254	7	ABD113975 Human pro
11	1369	100.0	1079	4	ABb74830 Prostate
12	1369	100.0	1079	4	ABU71860 Prostate
13	1364	99.6	254	3	AAB21320 Human pro
14	1364	99.6	254	4	Aay72525 Human pro
15	1364	99.6	254	5	AAU74901 Protein s
16	1364	99.6	254	5	Aau74932 Amino aci
17	1352	98.8	254	4	AAM01173 Human pro
18	1352	98.8	254	4	Aau69818 Human pro
19	1352	98.8	254	4	AG99058 Human pro
20	1352	98.8	254	4	ABU71709 Prostate
21	1352	98.8	254	5	ABb95278 Human P70
22	1352	98.8	254	6	ABR54390 Prostate
23	1352	98.8	254	7	ABD113973 Human mat
24	1352	98.8	258	3	ABb21324 Human EMS
25	1342	98.0	249	3	AAB21307 Human pro

ALIGNMENTS

RESULT 1
AAB21294
ID AAB21294 standard; protein; 254 AA.
XX
AC AAB21294;
XX
DT 02-FEB-2001 (first entry)
XX
DE Human KLK-L1 protein #2.
XX
KW Human, KLK-L1; KLK-L2; KLK-L3; KLK-L4; KLK-L5; KLK-L6;
KW kallikrein-like protein; serine protease; cytosolic; cancer;
KW prostate cancer.
XX
OS Homo sapiens.
XX
PN WC200053776-A2.
XX
PD 14-SEP-2000.
XX
PF 09-MAR-2000; 2000MO-CA0000258.
XX
PR 11-MAR-1999; 99US-0124260P.
PR 01-APR-1999; 99US-0127386P.
PR 21-JUL-1999; 99US-0144919P.
(MOUN) MOUNT SINAI HOSPITAL.
PI Yousef GM, Diamandis EP;
XX
DR WPI; 2000-587440/55.
DR N-PSDB; AAA95896.
XX
PT New kallikrein-like (KLK-L) proteins for diagnosing and treating KLK-L
protein mediated disorders, especially cancer.
XX
PS Claim 8; Page 141; 184pp; English.
XX
CC The present sequence is kallikrein-like protein KLK-L1. Kallikreins and
kallikrein-like proteins are a subgroup of the serine protease enzyme
family. They catalyze the selective cleavage of specific polypeptide
precursors to release peptides with potent biological activity. Nucleic
acids encoding kallikrein-like proteins KLK-L1, KLK-L2, KLK-L3, KLK-L4,
KLK-L5 and KLK-L6 have been isolated. The proteins are useful in the
treatment, monitoring and diagnosis of cancers, especially prostate
cancer. They can also be used to identify a substance that can associate
with or mediate the biological activity of the proteins. Antibodies can
be used to treat conditions mediated by the kallikrein-like proteins

26 1330 97.2 253 3 AAB21308 Human EMS
27 1255 91.7 234 4 AAE00397 Human ser
28 1241 90.7 231 2 AAY25510 Human pro
29 1237 90.4 237 3 AAB21293 Human KLK
30 1205 88.0 449 4 AAM01227 P703P and
31 1205 88.0 449 4 Aau69872 Human pro
32 1205 88.0 449 4 ABU71763 Prostate
33 1205 88.0 449 5 ABB95332 Human P70
34 1205 88.0 449 6 ABR54444 Prostate
35 1205 88.0 449 7 ABD14067 Human pro
36 1205 88.0 585 4 ABU71889 Prostate
37 1205 88.0 585 6 ABU71888 Prostate
38 1205 88.0 585 6 ABR54580 Prostate
39 1205 88.0 585 7 ABD14470 FOPP/hpAP
40 1205 88.0 801 4 ABU71890 Prostate
41 1191 87.0 226 4 AAY72526 Human pro
42 1191 87.0 226 5 AAU74902 Protein s
43 1191 87.0 226 5 AAU74933 Amino aci
44 1191 87.0 312 4 AAY72522 NS1-P703P
45 1191 87.0 312 5 AAU74768 Amino aci

XX SQ Sequence 254 AA;

Query Match 100.0%; Score 1369; DB 3; Length 254;

Best Local Similarity 100.0%; Pred. No. 6e-96;

Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATAGNPGWFLGYLLGVAGSLVSGSCQIINGEDCSPHSQPWOAALVMENELFCSGYL 60

DB 1 MATAGNPGWFLGYLLGVAGSLVSGSCQIINGEDCSPHSQPWOAALVMENELFCSGYL 60

QY 61 VHPQWLSAAHCFQNSYITIGLHSLVAGSLVSGSCQIINGEDCSPHSQPWOAALVMENELFCSGYL 120

DB 61 VHPQWLSAAHCFQNSYITIGLHSLVAGSLVSGSCQIINGEDCSPHSQPWOAALVMENELFCSGYL 120

QY 121 KLDESVSSEDRTIRSIASQCTAGNSCLVSGWGLLANGRMPTVLQCVNVSVSEVCSK 180

DB 121 KLDESVSSEDRTIRSIASQCTAGNSCLVSGWGLLANGRMPTVLQCVNVSVSEVCSK 180

QY 181 LYDPLVHPMFAGGQDQKSCNGDSGGPLICNGYLQGLVSGKAPCGQGVGVYTNL 240

DB 181 LYDPLVHPMFAGGQDQKSCNGDSGGPLICNGYLQGLVSGKAPCGQGVGVYTNL 240

QY 241 CKFTEWIEKTVQAS 254

DB 241 CKFTEWIEKTVQAS 254

RESULT 2

AAU01174

ID AAU01174 standard; protein; 254 AA.

AC AAU01174;

DT 04-OCT-2001 (first entry)

DE Human prostate-specific amino acid sequence P703P.

XX Human; prostate cancer; prostate-specific; diagnosis; vaccine;

KW cytostatic; gene therapy; metastasis.

XX Homo sapiens.

OS

XX WO200151633-A2.

PN 19-JUL-2001.

XX

XX 16-JAN-2001; 2001WO-US001574.

PF

XX 14-JAN-2000; 2000US-00483672.

PR

XX (CORI-) CORIXA CORP.

FA

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;

PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;

PI Wang A, Meagher WJ;

XX

XX WPI; 2001-425873/45.

DR

XX New polynucleotide encoding a prostate-specific protein, for diagnosing,

PT monitoring and treating prostate cancer in a patient and for use in

PT vaccines.

PT

XX

XX Claim 2; Page 405; 543pp; English.

PS

XX

XX The present invention describes polynucleotide sequences (I) which encode

CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,

CC and can be used in vaccine production and gene therapy. (I), (II),

CC antibodies to (II), fusion proteins comprising (II), and isolated T cells

CC prepared using (I) or (II) are used to treat cancer in a patient. (I) and

CC the antibodies are also used in the detection of cancer in a patient. The

CC cancer that is diagnosed or treated is particularly prostate cancer. (I)

CC and (II) can be used in vaccines. The antibodies or (I) can be used for

CC monitoring the progression of cancer in a patient. (I) and (II) can also

CC be used to improve diagnostic and therapeutic methods for prostate

CC cancer. They can indicate the level of metastasis as well as the prostate

CC volume. AAH93357 to AAH93944 and AAU01115 to AAU01118 represent

CC polynucleotide and amino acid sequences used in the exemplification of

CC the present invention

XX

SQ Sequence 254 AA;

Query Match 100.0%; Score 1369; DB 4; Length 254;

Best Local Similarity 100.0%; Pred. No. 6e-96; Indels 0; Gaps 0;

Matches 254; Conservative 0; Mismatches 0;

QY 1 MATAGNPGWFLGYLLGVAGSLVSGSCQIINGEDCSPHSQPWOAALVMENELFCSGYL 60

DB 1 MATAGNPGWFLGYLLGVAGSLVSGSCQIINGEDCSPHSQPWOAALVMENELFCSGYL 60

QY 61 VHPQWLSAAHCFQNSYITIGLHSLVAGSLVSGSCQIINGEDCSPHSQPWOAALVMENELFCSGYL 120

DB 61 VHPQWLSAAHCFQNSYITIGLHSLVAGSLVSGSCQIINGEDCSPHSQPWOAALVMENELFCSGYL 120

QY 121 KLDESVSSEDRTIRSIASQCTAGNSCLVSGWGLLANGRMPTVLQCVNVSVSEVCSK 180

DB 121 KLDESVSSEDRTIRSIASQCTAGNSCLVSGWGLLANGRMPTVLQCVNVSVSEVCSK 180

QY 181 LYDPLVHPMFAGGQDQKSCNGDSGGPLICNGYLQGLVSGKAPCGQGVGVYTNL 240

DB 181 LYDPLVHPMFAGGQDQKSCNGDSGGPLICNGYLQGLVSGKAPCGQGVGVYTNL 240

QY 241 CKFTEWIEKTVQAS 254

DB 241 CKFTEWIEKTVQAS 254

RESULT 3

AAU69819

ID AAU69819 standard; protein; 254 AA.

AC AAU69819;

XX 30-JAN-2002 (first entry)

DT Human prostate cDNA encoded protein #27.

DE Human; prostate cancer; cytostatic; immunostimulant; tumour; immunogen.

XX Homo sapiens.

OS

XX WO200173032-A2.

PN

XX 04-OCT-2001.

PD

XX 27-MAR-2001; 2001WO-US009919.

PF

XX 27-MAR-2000; 2000US-00536857.

PR 09-MAY-2000; 2000US-00568100.

PR 12-MAY-2000; 2000US-00570737.

PR 13-JUN-2000; 2000US-00593793.

PR 27-JUN-2000; 2000US-00605783.

PR 09-AUG-2000; 2000US-00638215.

PR 29-AUG-2000; 2000US-00651236.

PR 06-SEP-2000; 2000US-00657279.

PR 10-OCT-2000; 2000US-00679426.

PR 09-NOV-2000; 2000US-00709729.

XX (CORI-) CORIXA CORP.

PA

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;

PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedwick TS, Carter D;

PI Li SX, Wang A, Skeiky YAW, Hepler Wt, Henderson RA;

XX WPI; 2001-639232/73.

DR N-PSDB; AAS63914.
 XX New human prostate-specific polypeptides and polynucleotides useful for
 PT the diagnosis and treatment of cancer, especially prostate cancer.
 XX
 XX Claim 2; Page 405-406; 579pp; English.
 XX
 CC The invention relates to isolated prostate-specific polynucleotides,
 CC polypeptides, fusion proteins of the polypeptides, antibodies raised
 CC against the polypeptides (or antigenic epitopes derived from them) and
 CC antigen-presenting cells expressing the polypeptides. The antibodies are
 CC useful for detecting the presence of cancer, especially prostate cancer.
 CC The polypeptides, polynucleotides and the antigen-presenting cells are
 CC useful for stimulating and/or expanding T cells specific for a tumour
 CC protein, and for inhibiting the development of cancer especially prostate
 CC cancer. Compositions comprising the polynucleotide and/or polypeptide are
 CC useful for stimulating an immune response, and for treating cancer. The
 CC oligonucleotide is useful for detecting cancer. The present sequence is a
 CC prostate specific polypeptide of the invention
 XX
 SQ Sequence 254 AA;
 Query Match 100.0%; Score 1369; DB 4; Length 254;
 Best Local Similarity 100.0%; Pred. No. 6e-96;
 Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MATAGNFWGFLGYLLGVAGSLVSGSCQIINGDCSPHSQPMQAAALVMENELFCSGVL 60
 DB 1 MATAGNFWGFLGYLLGVAGSLVSGSCQIINGDCSPHSQPMQAAALVMENELFCSGVL 60
 QY 61 VHPQWVLSAAHCFQNSYTTIGLHLSLEADQEPGSMQVEASLSVRHPEYNRPLANDLMLI 120
 DB 61 VHPQWVLSAAHCFQNSYTTIGLHLSLEADQEPGSMQVEASLSVRHPEYNRPLANDLMLI 120
 QY 121 KLDESVSSEDTIRISIASQCTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEEVCSK 180
 DB 121 KLDESVSSEDTIRISIASQCTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEEVCSK 180
 QY 181 LYDPLVHPSMFCAGGGQDKSCNGDSGGPLICNGYLQGLVSPKAPCGQGVPGVYTNL 240
 DB 181 LYDPLVHPSMFCAGGGQDKSCNGDSGGPLICNGYLQGLVSPKAPCGQGVPGVYTNL 240
 QY 241 CKFTEWIEKTVQAS 254
 DB 241 CKFTEWIEKTVQAS 254
 RESULT 4
 AAG99059
 ID AAG99059 standard; protein; 254 AA.
 XX
 AC AAG99059;
 XX
 XX 25-SEP-2001 (first entry)
 DE Human prostate-specific amino acid of P703P.
 XX
 XX Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
 KW chromosome 22q11.2; prostate-specific protein; chromosome 1;
 KW prostate specific antigen; PSA.
 XX
 XX Homo sapiens.
 OS
 XX WO200134802-A2.
 XX
 XX 17-MAY-2001.
 XX
 XX 09-NOV-2000; 2000WO-US030904.
 PF
 XX 12-NOV-1999; 99US-00439313.
 PR 18-NOV-1999; 99US-00443686.
 XX
 XX (CORI-) CORIXA CORP.
 PA

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
 PI Kalos MD, Retter MW, Stolk JA, Day CH, Skeiky YAW, Wang A;
 XX WPI; 2001-308785/32.
 XX
 XX Isolated polypeptide comprising at least an immunogenic portion of a
 PT prostate-specific protein, useful in the diagnosis and therapy of
 PT prostate cancer.
 XX
 PS Claim 3; Page 304-305; 325pp; English.
 XX
 CC The present invention describes an isolated polypeptide (P1) comprising
 CC at least an immunogenic portion of a prostate-specific protein, or its
 CC variant. Also described are polynucleotides (N1) encoding (P1), (P1) and
 CC (N1) have cytostatic activity and can be used in vaccine production. The
 CC polypeptides, nucleic acids and antibodies from the present invention are
 CC useful in the diagnosis and therapy of prostate cancer. Prostate specific
 CC genes P704P, P712P, P774P, P775P and B305D are located in a genomic
 CC region on chromosome 22q11.2 known as the Cat Eye Syndrome region.
 CC Prostate specific antigen (PSA) P501S was located on chromosome 1.
 CC AAH84671 to AAH85143 and AAG99000 to AAG99077 represent polynucleotide
 CC and polypeptide sequences used in the exemplification of the present
 CC invention
 XX
 SQ Sequence 254 AA;
 Query Match 100.0%; Score 1369; DB 4; Length 254;
 Best Local Similarity 100.0%; Pred. No. 6e-96;
 Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MATAGNFWGFLGYLLGVAGSLVSGSCQIINGDCSPHSQPMQAAALVMENELFCSGVL 60
 DB 1 MATAGNFWGFLGYLLGVAGSLVSGSCQIINGDCSPHSQPMQAAALVMENELFCSGVL 60
 QY 61 VHPQWVLSAAHCFQNSYTTIGLHLSLEADQEPGSMQVEASLSVRHPEYNRPLANDLMLI 120
 DB 61 VHPQWVLSAAHCFQNSYTTIGLHLSLEADQEPGSMQVEASLSVRHPEYNRPLANDLMLI 120
 QY 121 KLDESVSSEDTIRISIASQCTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEEVCSK 180
 DB 121 KLDESVSSEDTIRISIASQCTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEEVCSK 180
 QY 181 LYDPLVHPSMFCAGGGQDKSCNGDSGGPLICNGYLQGLVSPKAPCGQGVPGVYTNL 240
 DB 181 LYDPLVHPSMFCAGGGQDKSCNGDSGGPLICNGYLQGLVSPKAPCGQGVPGVYTNL 240
 QY 241 CKFTEWIEKTVQAS 254
 DB 241 CKFTEWIEKTVQAS 254
 RESULT 5
 ABU71710
 ID ABU71710 standard; protein; 254 AA.
 XX
 AC ABU71710;
 XX
 XX 10-JUN-2003 (first entry)
 DT
 XX Prostate cancer specific antigen P703P #7.
 DE
 XX Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
 KW immunogen; cancer; prostate specific antigen.
 KW
 XX Homo sapiens.
 OS
 XX Synthetic.
 OS
 XX US2002192763-A1.
 PN
 XX 19-DEC-2002.
 PD
 XX 29-JUN-2001; 2001US-00895793.
 PF

```
XX 04-OCT-1999; 99US-0157455P.
PR 04-OCT-2000; 2000US-00679272.
PR 28-MAR-2001; 2001US-00822827.
XX (XUJ)/ XU J.
PA (DILL)/ DILLON D C.
PA (MITC)/ MITCHAM J L.
PA (HARL)/ HARLOCKER S L.
PA (JIAN)/ JIANG Y.
PA (KALO)/ KALOS M D.
PA (FANG)/ FANGER G R.
PA (RETT)/ RETTER M W.
PA (STOL)/ STOLK J A.
PA (DAYC)/ DAY C H.
PA (VEDV)/ VEDVICK T S.
PA (CART)/ CARTER D.
PA (LISX)/ LI S X.
PA (WANG)/ WANG A.
PA (SKEI)/ SKEIKY Y A W.
PA (HEPL)/ HEPLER W T.
PA (HEND)/ HENDERSON R A.
PA (HURA)/ HURAL J.
PA (MCNE)/ MCNEILL P D.
PA (HOUG)/ HOUGHTON R L.
PA (DBAS)/ Y DE BASSOLS C V.
PA (FOYT)/ FOY T M.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Rural J;
PI McNeill PD, Houghton RL, Y De Bassols CV, Foy TM;
XX
XX WPI; 2001-245062/25.
XX
XX Prostate specific protein and its encoding polynucleotide, useful for the
XX treatment and diagnosis of prostate cancer.
XX
XX Example 3; SEQ ID NO 525; 85pp; English.
XX
XX The invention describes a fusion protein comprising at least one amino
XX acid sequence of immunogenic portions of any of the 3 sequences not
XX defined in the specification, or sequences having at least 70 or 90 %
XX sequence identity to any one of the 35 sequences defined in the USPTO web
XX site, which is encoded by any of the 4 nucleotide sequences not defined
XX in the specification. The fusion protein, composition and methods are
XX useful for diagnosing, preventing and/or treating cancer, particularly
XX prostate cancer. The proteins are useful as markers to indicate the
XX presence or absence of cancer. This is the amino acid sequence of a
XX prostate cancer specific antigen. Note: The sequence data for this patent
XX did not form part of the printed specification, but was obtained in
XX electronic format directly from the US patent office at
XX seqdata.uspto.gov/sequence.html?DocID=US20020192763
XX
XX Sequence 254 AA;
XX
XX Query Match 100.0%; Score 1369; DB 4; Length 254;
XX Best Local Similarity 100.0%; Pred. No. 6e-96;
XX Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MATAGNPGWFLGYLILGVAGSLVSGSCSIINGSDCSPHQWQAALVMENELFCSGVL 60
XX
XX 1 MATAGNPGWFLGYLILGVAGSLVSGSCSIINGSDCSPHQWQAALVMENELFCSGVL 60
XX
XX 61 VHPQWLSNAHCFQNSYITIGLHSLQADQPGSQMVEASLSVRHPEYRPLLANDLMLI 120
XX
XX 61 VHPQWLSNAHCFQNSYITIGLHSLQADQPGSQMVEASLSVRHPEYRPLLANDLMLI 120
XX
XX 121 KLDESVSSEDTTIRSIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVEEVCCK 180
XX
XX 121 KLDESVSSEDTTIRSIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVEEVCCK 180
XX
XX 181 LYDPLYHPSMFCAGGQDQKSCNGDSGGPLICNGYLQGLVSGKAPCGQVGFVVTNL 240
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Db 181 LYDPLYHPSMFCAGGQDQKSCNGDSGGPLICNGYLQGLVSGKAPCGQVGFVVTNL 240
QY 241 CKTEWIEKTVQAS 254
Db 241 CKTEWIEKTVQAS 254
RESULT 6
ABB95279
ID ABB95279 standard; protein; 254 AA.
XX
XX ABB95279;
XX
XX 19-JUL-2002 (first entry)
XX
XX Human P703P putative full length protein SEQ ID NO 525.
XX
XX Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
XX Gene therapy.
XX
XX Homo sapiens.
XX
XX US2002022248-A1.
XX
XX 21-FEB-2002.
XX
XX 12-JAN-2001; 2001US-00759143.
XX
XX 25-FEB-1997; 97US-00806099.
XX 01-AUG-1997; 97US-00904804.
XX 10-FEB-1998; 98US-00020956.
XX 25-FEB-1998; 98US-00030607.
XX 14-JUL-1998; 98US-00115453.
XX 23-SEP-1998; 98US-00159812.
XX 15-JAN-1999; 99US-00232149.
XX 09-APR-1999; 99US-00288946.
XX 13-JUL-1999; 99US-00352616.
XX 12-NOV-1999; 99US-00439313.
XX 18-NOV-1999; 99US-00433686.
XX 14-JAN-2000; 2000US-00483672.
XX 27-MAR-2000; 2000US-00536857.
XX 09-MAY-2000; 2000US-00568100.
XX 12-MAY-2000; 2000US-00570737.
XX 13-JUN-2000; 2000US-00593793.
XX 27-JUN-2000; 2000US-00605783.
XX 10-AUG-2000; 2000US-00636215.
XX 29-AUG-2000; 2000US-00651236.
XX 06-SEP-2000; 2000US-00657279.
XX 02-OCT-2000; 2000US-00679426.
XX 10-OCT-2000; 2000US-00685166.
XX (XUJ)/ XU J.
XX (DILL)/ DILLON D C.
XX (MITC)/ MITCHAM J L.
XX (HARL)/ HARLOCKER S L.
XX (JIAN)/ JIANG Y.
XX (KALO)/ KALOS M D.
XX (FANG)/ FANGER G R.
XX (RETT)/ RETTER M W.
XX (STOL)/ STOLK J A.
XX (DAYC)/ DAY C H.
XX (VEDV)/ VEDVICK T S.
XX (CART)/ CARTER D.
XX (LISX)/ LI S X.
XX (WANG)/ WANG A.
XX (SKEI)/ SKEIKY Y A W.
XX (HEPL)/ HEPLER W T.
XX (HEND)/ HENDERSON R A.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
XX Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
XX Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
```

XX WP1; 2002-255649/30.
XX New prostate-specific polynucleotides for diagnosing and treating
XX diseases, in particular prostate cancer, and as markers for the
PT progression of cancer.
XX
XX Claim 2; SEQ ID NO 525; 87pp; English.
XX
XX The present invention provides prostate-specific coding sequences and
XX their encoded proteins. These can be used in the diagnosis and treatment
XX of cancers, particularly prostate cancer. The present sequence is a
XX protein described in the invention
XX
XX Sequence 254 AA;
SQ
Query Match 100.0%; Score 1369; DB 5; Length 254;
Best Local Similarity 100.0%; Pred. No. 6e-96;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATAGNPGWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWQAALVMENELFCSGVL 60
Db 1 MATAGNPGWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWQAALVMENELFCSGVL 60
QY 61 VHPQWVLSAAHCFQNSYITIGLHLSLEADQEPGSMVEASLSVRHPEYNRPILLANDLMLI 120
Db 61 VHPQWVLSAAHCFQNSYITIGLHLSLEADQEPGSMVEASLSVRHPEYNRPILLANDLMLI 120
QY 121 KLDESVSSEDITRISIASQCPTAGNSCLVSGWGLLANGRMPTVLCQNVSVVSEEVCSK 180
Db 121 KLDESVSSEDITRISIASQCPTAGNSCLVSGWGLLANGRMPTVLCQNVSVVSEEVCSK 180
QY 181 LYDPLYHPSMFCAGGQDQKSCNGSDGGPLICNGYLGVLSPGKAPCGQVGPVYTNL 240
Db 181 LYDPLYHPSMFCAGGQDQKSCNGSDGGPLICNGYLGVLSPGKAPCGQVGPVYTNL 240
QY 241 CKFTEWIEKTVQAS 254
Db 241 CKFTEWIEKTVQAS 254
RESULT 7
ABP54360
ID ABP54360 standard; protein; 254 AA.
XX
XX AC ABP54360;
XX
XX DT 20-JAN-2003 (first entry)
XX
XX DE Human KLK4 protein SEQ ID NO:13.
XX
XX KW Human; KLK4; cancer; benign tumour; cytostatic4.
XX
XX OS Homo sapiens.
XX
XX PN WO200277243-A1.
XX
XX PD 03-OCT-2002.
XX
XX PF 27-MAR-2002; 2002WO-AU0000378.
XX
XX PR 27-MAR-2001; 2001AU-00004022.
XX
XX PA (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
XX
XX PI Dong Y, Clements JA;
XX
XX DR WPI; 2003-029939/02.
XX
XX DR N-PSDB; ASQ83347.
XX
XX Detecting the presence or diagnosing the risk of cancer or benign tumor,
PT e.g. an ovarian, endometrial or prostate cancer, by determining the
PT presence of or detecting aberrant expression of KLK4 in a biological

PT sample from the patient.
XX
XX Disclosure; Page 118-119; 126pp; English.
XX
XX The present invention describes a method (M1) for detecting the presence
XX of diagnosing the risk of cancer or benign tumour in a patient. M1
XX comprises determining the presence of or detecting aberrant expression of
XX KLK4 in a biological sample obtained from the patient. KLK4 has
XX cytostatic activity. The method is useful for detecting the presence or
XX diagnosing the risk of a cancer or a benign tumour in a patient,
XX particularly an ovarian, endometrial or prostate cancer, or a cancer or
XX benign tumour associated with an organ or tissue from the ovaries,
XX endometrium or prostate. An agent which can be used for restoring or
XX modulating KLK4 expression can be used for treating or preventing cancer
XX or benign tumour. KLK4 polynucleotides, polypeptides or antigen-binding
XX molecules from the present invention can be used for detecting aberrant
XX KLK4 polynucleotides or aberrant K4 polypeptides that correlate with a
XX cancer or a benign tumour. The present sequence represents human KLK4
XX from the present invention
XX
XX Sequence 254 AA;
SQ
Query Match 100.0%; Score 1369; DB 6; Length 254;
Best Local Similarity 100.0%; Pred. No. 6e-96;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATAGNPGWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWQAALVMENELFCSGVL 60
Db 1 MATAGNPGWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWQAALVMENELFCSGVL 60
QY 61 VHPQWVLSAAHCFQNSYITIGLHLSLEADQEPGSMVEASLSVRHPEYNRPILLANDLMLI 120
Db 61 VHPQWVLSAAHCFQNSYITIGLHLSLEADQEPGSMVEASLSVRHPEYNRPILLANDLMLI 120
QY 121 KLDESVSSEDITRISIASQCPTAGNSCLVSGWGLLANGRMPTVLCQNVSVVSEEVCSK 180
Db 121 KLDESVSSEDITRISIASQCPTAGNSCLVSGWGLLANGRMPTVLCQNVSVVSEEVCSK 180
QY 181 LYDPLYHPSMFCAGGQDQKSCNGSDGGPLICNGYLGVLSPGKAPCGQVGPVYTNL 240
Db 181 LYDPLYHPSMFCAGGQDQKSCNGSDGGPLICNGYLGVLSPGKAPCGQVGPVYTNL 240
QY 241 CKFTEWIEKTVQAS 254
Db 241 CKFTEWIEKTVQAS 254
RESULT 8
ABP54357
ID ABP54357 standard; protein; 254 AA.
XX
XX AC ABP54357;
XX
XX DT 20-JAN-2003 (first entry)
XX
XX DE Human KLK4 protein SEQ ID NO:6.
XX
XX KW Human; KLK4; cancer; benign tumour; cytostatic.
XX
XX OS Homo sapiens.
XX
XX PN WO200277243-A1.
XX
XX PD 03-OCT-2002.
XX
XX PF 27-MAR-2002; 2002WO-AU0000378.
XX
XX PR 27-MAR-2001; 2001AU-00004022.
XX
XX PA (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
XX
XX PI Dong Y, Clements JA;
XX
XX

DR WPI: 2003-029939/02.
 DR N-PSDB; ASQ83343.
 XX
 PT Detecting the presence or diagnosing the risk of cancer or benign tumor,
 PT e.g. an ovarian, endometrial or prostate cancer, by determining the
 PT presence of or detecting aberrant expression of KLK4 in a biological
 PT sample from the patient.
 XX
 PS Disclosure; Fig 3; 126pp; English.
 XX
 CC The present invention describes a method (M1) for detecting the presence
 CC or diagnosing the risk of cancer or benign tumor in a patient. M1
 CC comprises determining the presence of or detecting aberrant expression of
 CC KLK4 in a biological sample obtained from the patient. KLK4 has
 CC cytotatic activity. The method is useful for detecting the presence or
 CC diagnosing the risk of a cancer or a benign tumor in a patient, or
 CC particularly an ovarian, endometrial or prostate cancer, or a cancer or
 CC benign tumor associated with an organ or tissue from the ovaries,
 CC endometrium or prostate. An agent which can be used for restoring or
 CC modulating KLK4 expression can be used for treating or preventing cancer
 CC or benign tumor. KLK4 polynucleotides, polypeptides or antigen-binding
 CC molecules from the present invention can be used for detecting aberrant
 CC KLK4 polynucleotides or aberrant K4 polypeptides that correlate with a
 CC cancer or a benign tumor. The present sequence represents human KLK4
 CC from the present invention
 XX
 SQ Sequence 254 AA;

Query Match 100.0%; Score 1369; DB 6; Length 254;
 Best Local Similarity 100.0%; Pred. No. 6e-96;
 Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NATAGNPGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPWOAALVMENELFCSGVL 60
 Db 1 NATAGNPGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPWOAALVMENELFCSGVL 60
 QY 61 VHPQWLSAACHFQNSYITGLGHSLEADQEPGQWVEASLSVRHPEYNRPRLANDLMLI 120
 Db 61 VHPQWLSAACHFQNSYITGLGHSLEADQEPGQWVEASLSVRHPEYNRPRLANDLMLI 120
 QY 121 KLDESVSDDTIRSIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
 Db 121 KLDESVSDDTIRSIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
 QY 181 LYDPLYPHSMFCAGGQDQKSCNGDSGGPLICNGYLQGLVSGKAPCGQVGPVYTNL 240
 Db 181 LYDPLYPHSMFCAGGQDQKSCNGDSGGPLICNGYLQGLVSGKAPCGQVGPVYTNL 240
 QY 241 CKFTIEWIKTVQAS 254
 Db 241 CKFTIEWIKTVQAS 254

RESULT 9
 ABR54391
 ID ABR54391 standard; protein; 254 AA.
 XX
 AC ABR54391;
 XX
 DT 28-AUG-2003 (first entry)
 XX
 DE Prostate tumour specific protein sequence SEQ ID 525.
 XX
 KW Cytostatic; gene therapy; prostate-specific protein; P5P; human;
 KW immune response; prostate cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200289747-A2.
 XX
 PD 14-NOV-2002.
 XX
 PF 09-MAY-2002; 2002WO-US014753.

XX
 PR 09-MAY-2001; 2001US-00852911.
 PR 29-JUN-2001; 2001US-00895814.
 PR 10-DEC-2001; 2001US-00012896.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 XU J. Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
 PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
 PI Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
 PI McNeill PD, Houghton RL, Vinals Y De Bassolac, Foy TM, Watanabe Y;
 PI Deng T;
 XX
 DR WPI: 2003-167130/16.
 XX
 PT New prostate-specific proteins and genes, useful in gene therapy,
 PT particularly for stimulating an immune response in a patient, or treating
 PT prostate cancer in a patient, as well as for diagnosing prostate cancer
 PT in a patient.
 XX
 PS Example 3; Page 472; 691pp; English.
 XX
 CC The present invention relates to novel prostate-specific proteins (PSP)
 CC and their coding sequences. The PSPs and their coding sequences are
 CC useful for stimulating an immune response in a patient, or for treating
 CC prostate cancer in a patient and for determining, detecting or diagnosing
 CC the presence of a cancer in a patient. The present sequence was used to
 CC illustrate the invention
 XX
 SQ Sequence 254 AA;

Query Match 100.0%; Score 1369; DB 6; Length 254;
 Best Local Similarity 100.0%; Pred. No. 6e-96;
 Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATAGNPGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPWOAALVMENELFCSGVL 60
 Db 1 MATAGNPGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPWOAALVMENELFCSGVL 60
 QY 61 VHPQWLSAACHFQNSYITGLGHSLEADQEPGQWVEASLSVRHPEYNRPRLANDLMLI 120
 Db 61 VHPQWLSAACHFQNSYITGLGHSLEADQEPGQWVEASLSVRHPEYNRPRLANDLMLI 120
 QY 121 KLDESVSDDTIRSIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
 Db 121 KLDESVSDDTIRSIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
 QY 181 LYDPLYPHSMFCAGGQDQKSCNGDSGGPLICNGYLQGLVSGKAPCGQVGPVYTNL 240
 Db 181 LYDPLYPHSMFCAGGQDQKSCNGDSGGPLICNGYLQGLVSGKAPCGQVGPVYTNL 240
 QY 241 CKFTIEWIKTVQAS 254
 Db 241 CKFTIEWIKTVQAS 254

RESULT 10
 ADB13975
 ID ADB13975 standard; protein; 254 AA.
 XX
 AC ADB13975;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human prostate specific protein P703P.
 XX
 KW Human; prostate specific cDNA; cytostatic; immunostimulant; gene therapy;
 KW cell therapy; vaccine; T-cell epitope;
 KW class I major histocompatibility complex allele; MHC; prostate cancer;
 KW tumour; antigen presenting cell.
 XX
 OS Homo sapiens.

PN US2003185830-A1.
XX 02-OCT-2003.
PD 12-NOV-2002; 2002US-00294025.
XX 25-FEB-1997; 97US-00806099.
XX 01-AUG-1997; 97US-00304804.
XX 09-FEB-1998; 98US-00202956.
XX 25-FEB-1998; 98US-00030607.
XX 14-JUL-1998; 98US-00115453.
XX 23-SEP-1998; 98US-00159812.
XX 15-JAN-1999; 99US-00232149.
XX 09-APR-1999; 99US-00288946.
XX 13-JUL-1999; 99US-00352616.
XX 12-NOV-1999; 99US-00439313.
XX 18-NOV-1999; 99US-00434686.
XX 14-JAN-2000; 2000US-00483672.
XX 27-MAR-2000; 2000US-00536857.
XX 09-MAY-2000; 2000US-00568100.
XX 12-MAY-2000; 2000US-00570737.
XX 13-JUN-2000; 2000US-00593793.
XX 27-JUN-2000; 2000US-00605783.
XX 09-AUG-2000; 2000US-00626215.
XX 29-AUG-2000; 2000US-00651236.
XX 06-SEP-2000; 2000US-00657279.
XX 02-OCT-2000; 2000US-00679426.
XX 10-OCT-2000; 2000US-00685166.
XX 09-NOV-2000; 2000US-00709729.
XX 12-JAN-2001; 2001US-00759143.
XX 09-FEB-2001; 2001US-00780669.
XX 29-JUN-2001; 2001US-00852911.
XX 10-DEC-2001; 2001US-00895814.
XX 09-MAY-2002; 2002US-00012896.
XX 09-MAY-2002; 2002US-00146678.
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Stolk JA, Kalos MD;
XX WPI; 2003-756193/71.
XX N-PSDB; ADB13974.
XX
XX New isolated polypeptide for use in a vaccine for stimulating an immune
XX response, or for treating or diagnosis cancer, preferably prostate
XX cancer.
XX
XX Example 3; Page; 101pp; English.
XX
XX The invention relates to an isolated polypeptide comprising no more than
XX 11-542 amino acids of ADB13563 comprising a sequence ADB1487. The
XX peptides comprise a fragment ADB13563 of that contain naturally processed
XX T-cell epitopes for 3 class I major histocompatibility complex (MHC)
XX alleles. ADB13563 is a polypeptide encoded by a human prostate specific
XX cDNA, one of 648 disclosed as new. Also included are nucleic acids
XX encoding the proteins and peptides, expression vectors, a host cell
XX transformed with the vector, an isolated antibody (or antigen binding
XX fragment) that specifically binds to the protein or peptide, detecting
XX the presence of a cancer in a patient (comprising contacting a patient
XX sample with a binding agent that binds to the peptides or a polypeptide
XX appearing as ADB1358, detecting the amount of polypeptide that binds to
XX the agent and comparing the amount of polypeptide to a predetermined cut-
XX off value to determine the presence of cancer), a fusion protein
XX comprising the peptides or proteins, stimulating or expanding T cells
XX specific for a tumour protein comprising contacting T cells with the
XX peptides or the isolated T cell population, treating prostate cancer in a
XX patient comprising administering a composition comprising the peptides,
XX nucleic acids, antibodies or compounds, determining the presence of a
XX cancer in a patient and treating prostate cancer in a patient comprising
XX incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated
XX from a patient with the peptides or antigen presenting cells that express
XX (the peptides so that the T cells proliferate, and administering the
XX proliferated T cells to the patient. The peptides (or an oligonucleotide

CC that hybridises to nucleic acid encoding them), is used to detect the
CC presence of cancer in a patient. The peptides, nucleic acids encoding, or
CC antigen-presenting cells expressing the nucleic acid, are used to
CC stimulate or expand T cells specific for a tumour protein. The peptides,
CC nucleic acids, antibodies, fusion proteins, T cell populations or antigen
CC presenting cells are used to stimulate an immune response or treat
CC prostate cancer in a patient. The present sequence is a prostate specific
CC protein of the invention. Note: Except where otherwise indicated, the
CC sequence data for this patent did not form part of the printed, the
CC specification, but was obtained in electronic format directly from USPTO
XX at seqdata.uspto.gov/sequence.html?DocID=20030185830.
XX
XX Sequence 254 AA;
XX
XX Query Match 100.0%; Score 1369; DB 7; Length 254;
XX Best Local Similarity 100.0%; Pred. No. 6e-96; Indels 0; Gaps 0;
XX Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATAGNPMGWFLGYLILGVAGSLVSGSCSIINGEDCSFHSQPMQAAALVMENELFCSGVL 60
DB 1 MATAGNPMGWFLGYLILGVAGSLVSGSCSIINGEDCSFHSQPMQAAALVMENELFCSGVL 60
QY 61 VHPQWVLSNAHCFOFNSYTGILGHSLEADQBPQSGQVSEASLVRHPEYNRPILLANDLMLI 120
DB 61 VHPQWVLSNAHCFOFNSYTGILGHSLEADQBPQSGQVSEASLVRHPEYNRPILLANDLMLI 120
QY 121 KLDESVSESDTIRISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
DB 121 KLDESVSESDTIRISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
QY 181 LYDPLYPHSMFCAGGQKQKSCNODSGGPLICNGLYSGFKAPCGQVGVGYTNL 240
DB 181 LYDPLYPHSMFCAGGQKQKSCNODSGGPLICNGLYSGFKAPCGQVGVGYTNL 240
QY 241 CKFTWIEKTVQAS 254
DB 241 CKFTWIEKTVQAS 254
XX
XX RESULT 11
XX AAB74830
XX ID AAB74830 standard; protein; 1079 AA.
XX
XX AC AAB74830;
XX
XX DT 14-JUN-2001 (first entry)
XX
XX DE Prostate tumour antigen amino acid sequence for a fusion protein.
XX
XX KM Human; prostate tumour antigen; prostate tumour; therapy; diagnosis;
XX prostate cancer; immunogenic; cytostatic; vaccine.
XX
XX OS Homo sapiens.
XX
XX PN WO200125272-A2.
XX
XX PD 12-APR-2001.
XX
XX PF 04-OCT-2000; 2000WO-US027464.
XX
XX PR 04-OCT-1999; 99US-0157455P.
XX
XX PA (CORI-) CORIXA CORP.
XX
XX PI Xu J, Skeiky YAW, Reed SG, Cheever MA;
XX WPI; 2001-245062/25.
XX
XX PT Prostate specific protein and its encoding polynucleotide, useful for the
XX treatment and diagnosis of prostate cancer.
XX
XX PS Disclosure; Page 272-276; 276pp; English.
XX

CC The present invention describes an isolated polypeptide (I) comprising at
 CC least an immunogenic portion of a prostate tumour antigen protein or its
 CC variant. (I) have cytostatic activity and can be used in vaccine
 CC production. (I), prostate tumour antigen polynucleotides, an antigen
 CC presenting cell (APC e.g. a dendritic cell) that expresses (I), and a
 CC pharmaceutical composition containing (I) are useful for inhibiting the
 CC development of cancer in a patient. Antibodies specific for prostate
 CC specific proteins and oligonucleotides that hybridise to a polynucleotide
 CC that encodes a prostate specific protein are useful for detecting the
 CC presence or absence of a cancer or monitoring the progression the
 CC progression of a cancer, especially prostate cancer. AAH02422 to AAH2872,
 CC AAH74798 to AAH74821 and AAH74830 are sequences used in the
 CC exemplification of the present invention

XX Sequence 1079 AA;

Query Match 100.0%; Score 1369; DB 4; Length 1079;
 Best Local Similarity 100.0%; Pred. No. 2.6e-95;
 Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATAGNPGWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPQWQAALVMENELFCSGVL 60
 DB 271 MATAGNPGWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPQWQAALVMENELFCSGVL 330
 QY 61 VHPQWLVAARCFQNSYITIGLHSLADQEPGQSQWVEASLSVRHPEYRNPRLANDLMLI 120
 DB 331 VHPQWLVAARCFQNSYITIGLHSLADQEPGQSQWVEASLSVRHPEYRNPRLANDLMLI 390
 QY 121 KLDSESVESDTRISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVEVCSK 180
 DB 391 KLDSESVESDTRISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVEVCSK 450
 QY 181 LYDPLYHPSMFCAGGQDQKDCNGDSGGPLICNGYLQGLVSGFKAPCGQGVPGVYTNL 240
 DB 451 LYDPLYHPSMFCAGGQDQKDCNGDSGGPLICNGYLQGLVSGFKAPCGQGVPGVYTNL 510
 QY 241 CKFTEWIEKTVQAS 254
 DB 511 CKFTEWIEKTVQAS 524

RESULT 12

ABU71860
 ID ABU71860 standard; protein; 1079 AA.

AC ABU71860;

XX 10-JUN-2003 (first entry)

DE Prostate specific antigen fusion protein #2.

KW Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
 KW immunogen; cancer; prostate specific antigen; PSA;
 KW prostatic acid phosphatase; PAP; prostate specific membrane antigen;
 KW PSMA.

XX Homo sapiens.

OS Synthetic.

XX US2002192763-A1.

XX 19-DEC-2002.

PF 29-JUN-2001; 2001US-00895793.

XX 04-OCT-1999; 99US-0157455P.

PR 04-OCT-2000; 2000US-00679272.

PR 28-MAR-2001; 2001US-00822827.

XX (XUJ/) XU J.

PA (DILL/) DILLON D C.

PA (MITC/) MITCHAM J L.

PA (HARL/) HARLOCKER S L.

PA (JIAN/) JIANG Y.
 PA (KALO/) KALOS M D.
 PA (FANG/) FANGER G R.
 PA (RETT/) RETTER M W.
 PA (STOL/) STOLK J A.
 PA (DAYC/) DAY C H.
 PA (VEDV/) VEDVICK T S.
 PA (CART/) CARTER D.
 PA (LISK/) LI S X.
 PA (WANG/) WANG A.
 PA (SKEI/) SKEIKY Y A W.
 PA (HEPL/) HEPLER W T.
 PA (HEND/) HENDERSON R A.
 PA (HURA/) HURAL J.
 PA (MCNE/) MCNEILL P D.
 PA (HOUG/) HOUGHTON R L.
 PA (DBAS/) Y DE BASSOLS C V.
 PA (FOYT/) FOY T M.

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
 PI Li SX, Wang A, Skeiky YAM, Hepler WT, Henderson RA, Hural J;
 PI McNeill PD, Houghton RL, Y De BassolsCV, Foy TM;

XX WPI; 2001-245062/25.

XX Prostate specific protein and its encoding polynucleotide, useful for the
 PT treatment and diagnosis of prostate cancer.

XX Claim 5; SEQ ID NO 947; 85pp; English.

XX The invention describes a fusion protein comprising at least one amino
 CC acid sequence of immunogenic portions of any of the 3 sequences not
 CC defined in the specification, or sequences having at least 70 or 90 %
 CC sequence identity to any one of the 35 sequences defined in the USPTO web
 CC site, which is encoded by any of the 4 nucleotide sequences not defined
 CC in the specification. The fusion protein, composition and methods are
 CC useful for diagnosing, preventing and/or treating cancer, particularly
 CC prostate cancer. The proteins are useful as markers to indicate the
 CC presence or absence of cancer. This is the amino acid sequence of a
 CC fusion protein of the invention created from fragments of prostate
 CC specific antigen (PSA), prostatic acid phosphatase (PAP), prostatic
 CC specific membrane antigen (PSMA) and prostate specific antigens of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from the US patent office at
 CC seqdata.uspto.gov/sequence.html?DocID=US20020192763

XX Sequence 1079 AA;

Query Match 100.0%; Score 1369; DB 4; Length 1079;

Best Local Similarity 100.0%; Pred. No. 2.6e-95;
 Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATAGNPGWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPQWQAALVMENELFCSGVL 60
 DB 271 MATAGNPGWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPQWQAALVMENELFCSGVL 330
 QY 61 VHPQWLVAARCFQNSYITIGLHSLADQEPGQSQWVEASLSVRHPEYRNPRLANDLMLI 120
 DB 331 VHPQWLVAARCFQNSYITIGLHSLADQEPGQSQWVEASLSVRHPEYRNPRLANDLMLI 390
 QY 121 KLDSESVESDTRISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVEVCSK 180
 DB 391 KLDSESVESDTRISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVEVCSK 450
 QY 181 LYDPLYHPSMFCAGGQDQKDCNGDSGGPLICNGYLQGLVSGFKAPCGQGVPGVYTNL 240
 DB 451 LYDPLYHPSMFCAGGQDQKDCNGDSGGPLICNGYLQGLVSGFKAPCGQGVPGVYTNL 510
 QY 241 CKFTEWIEKTVQAS 254
 DB 511 CKFTEWIEKTVQAS 524

RESULT 13

AAB21320
ID AAB21320 standard; protein; 254 AA.XX
AC AAB21320;XX
DT 02-FEB-2001 (first entry)XX
DE Human prostate.XX
KW Human; KLK-L1; KLK-L2; KLK-L3; KLK-L4; KLK-L5; KLK-L6; prostate;
KW kallikrein-like protein; serine protease; cytostatic; cancer;
KW prostate cancer.XX
OS Homo sapiens.XX
PN W0200053776-A2.XX
PD 14-SEP-2000.XX
PF 09-MAR-2000; 2000WO-CA000258.XX
PR 11-MAR-1999; 99US-0124260P.XX
PR 01-APR-1999; 99US-0127386P.XX
PR 21-JUL-1999; 99US-0144919P.XX
FA (MOUN) MOUNT SINAI HOSPITAL.XX
FI Yousef GM, Diamandis EP;XX
XX WPI; 2000-587440/55.XX
PT New kallikrein-like (KLK-L) proteins for diagnosing and treating KLK-L
PT protein mediated disorders, especially cancer.XX
PS Example 4; Fig 17; 184pp; English.XX
CC The present sequence is human prostate, a member of the serine protease
CC family. Kallikreins and kallikrein-like proteins are a subgroup of the
CC serine protease enzyme family. They catalyse the selective cleavage of
CC specific polypeptide precursors to release peptides with potent
CC biological activity. Nucleic acids encoding kallikrein-like proteins KLK-
CC L1, KLK-L2, KLK-L3, KLK-L4, KLK-L5 and KLK-L6 have been isolated. The
CC proteins are useful in the treatment, monitoring and diagnosis of
CC cancers, especially prostate cancer. They can also be used to identify a
CC substance that can associate with or mediate the biological activity of
CC the proteins. Antibodies can be used to treat conditions mediated by the
CC kallikrein-like proteinsXX
SQ Sequence 254 AA;

Query Match 99.6%; Score 1364; DB 3; Length 254;

Best Local Similarity 99.6%; Pred. No. 1.4e-95;

Matches 253; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATAGNPMGFWLGLYLLGVAGSLVSGSCQIINGEDCSPHSQPQWQAALVMENELFCSGVL 60

DB 1 MATAGNPMGFWLGLYLLGVAGSLVSGSCQIINGEDCSPHSQPQWQAALVMENELFCSGVL 60

QY 61 VHPQWVLSAHCQNSYTIIGLHLSLEADQPGSQMVEASLSVRHPEYNRPPLANDLMLI 120

DB 61 VHPQWVLSAHCQNSYTIIGLHLSLEADQPGSQMVEASLSVRHPEYNRPPLANDLMLI 120

QY 121 KLDESVESEDTIRISIASQCPAGNSCLVSGWGLLANGRMPTVLCQNVSVVSEVCSK 180

DB 121 KLDESVESEDTIRISIASQCPAGNSCLVSGWGLLANGRMPTVLCQNVSVVSEVCSK 180

QY 181 LYDPLXHPNFCAGGQDQKDCNNGSGGPLICNGYLQGLVSPGKAPCGQGVPGVYTNL 240

DB 181 LYDPLXHPNFCAGGQDQKDCNNGSGGPLICNGYLQGLVSPGKAPCGQGVPGVYTNL 240

QY 241 CKFTIEWIEKTVQAS 254
DB 241 CKFTIEWIEKTVQAS 254

RESULT 14

AAY72525

ID AAY72525 standard; protein; 254 AA.

XX
AC AAY72525;XX
DT 02-MAY-2001 (first entry)XX
DE Human prostate antigen #3.XX
KW Human; prostate; P703P; gene therapy; prostate cancer; cytostatic; PIN;
KW prostate intraepithelial neoplasia; NSI; non-structural protein; vaccine;
KW haemagglutinin; prostatic hyperplasia; prostate-specific serine protease;
KW therapy.XX
OS Homo sapiens.XX
PN W0200104143-A2.XX
PD 18-JAN-2001.XX
PF 11-JUL-2000; 2000WO-EP006618.XX
PR 13-JUL-1999; 99US-00352616.XX
PR 12-NOV-1999; 99US-00439313.XX
PR 18-NOV-1999; 99US-00443686.XX
PR 14-JAN-2000; 2000US-00483672.XX
PR 27-MAR-2000; 2000US-00536857.XX
PR 09-MAY-2000; 2000US-00568100.XX
PR 12-MAY-2000; 2000US-00570737.XX
PR 13-JUN-2000; 2000US-00593793.XX
PR 27-JUN-2000; 2000GB-00015747.XX
PR 27-JUN-2000; 2000US-00605783.XX
PA (SMIX) SMITHKLINE BEECHAM BIOLOGICALS.
PA (CORI-) CORIXA CORP.XX
PI Cabezón Silva T, Dillon DC;XX
DR WPI; 2001-159380/16.XX
PT New prostate protein or its fragment linked to a immunological/expression
PT enhancer fusion partner, useful for preparing vaccines for treating
PT prostate cancers or prostate associated tumors.XX
PS Claim 2; Page 49; 50pp; English.XX
CC The present protein sequence is a human prostate antigen. The invention
CC relates to a prostate protein (prostate-specific serine protease) or its
CC fragment fused to an immunological or an expression enhancer fusion
CC partner, such as NSI (haemagglutinin). The fusion protein is used for
CC formulating vaccines useful for immunotherapeutically treating patients
CC susceptible to or suffering from prostate-cancer and prostate-expressing
CC tumours other than prostate tumours, prostatic hyperplasia and prostate
CC intraepithelial neoplasia (PIN). Genetic constructs containing prostate
CC nucleic acids are also useful in gene therapy techniques to induce an
CC immune responseXX
SQ Sequence 254 AA;

Query Match 99.6%; Score 1364; DB 4; Length 254;

Best Local Similarity 99.6%; Pred. No. 1.4e-95;

Matches 253; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATAGNPMGFWLGLYLLGVAGSLVSGSCQIINGEDCSPHSQPQWQAALVMENELFCSGVL 60

DB 1 MATAGNPMGFWLGLYLLGVAGSLVSGSCQIINGEDCSPHSQPQWQAALVMENELFCSGVL 60

QY 61 VHPQWLSAAHCFQNSYITIGLHLSLEADQEPGSMVEASLSVRHPEYNRPPLANDLMLI 120
DB 61 VHPQWLSAAHCFQNSYITIGLHLSLEADQEPGSMVEASLSVRHPEYNRPPLANDLMLI 120
QY 121 KLDESVSSESDTIRISISIASOCPAGNSCLVSGWGLLANGRMPTVLOCVNVSVVSEEVCSK 180
DB 121 KLDESVSSESDTIRISISIASOCPAGNSCLVSGWGLLANGRMPTVLOCVNVSVVSEEVCSK 180
QY 181 LYDPLYHPSMFCAGGQDQKDSNGDSGGPLICNGYLQGLVSGKAPCGQGVGVVYTNL 240
DB 181 LYDPLYHPSMFCAGGQDQKDSNGDSGGPLICNGYLQGLVSGKAPCGQGVGVVYTNL 240
QY 241 CKFTIEWIEKTVQAS 254
DB 241 CKFTIEWIEKTVQAS 254

RESULT 15

AAU74901
ID AAU74901 standard; protein: 254 AA.

AC AAU74901;

XX 09-APR-2002 (first entry)

XX Protein sequence of prostate homologue #3.

XX Human; cytostatic; immunostimulant; vaccine; prostate antigen;
KW prostate cancer; prostate-specific serine protease;
KW prostate-associated tumour.

OS Homo sapiens.

PN WO200200708-A2.

PD 03-JAN-2002.

XX 21-JUN-2001; 2001WO-EP007079.

XX 27-JUN-2000; 2000GB-00015736.

XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

XX Cabezón Silva TEV, Marchand M, Vinals Y De BassolsC;

XX WPI; 2002-147879/19.

XX Prostate antigen derivative carrying a mutation in the active site useful
PT manufacture of a vaccine for treating a patient suffering from prostate
PT cancer or other prostate-associated tumors.

PS Disclosure; Page 62; 65pp; English.

XX The present invention relates to a new prostate antigen derivative where
CC the prostate sequence is carrying a mutation in the active site of the
CC protein. The molecules of the invention may be used for the manufacture
CC of a vaccine for treating a patient suffering from prostate cancer or
CC other prostate-associated tumors. The present amino acid sequence
CC represents one of a collection of prostate homologues (AAU74769-AAU74770
CC and AAU74901-AAU74902) of the invention. The homologues were used in the
CC invention to create mutant prostate sequences (AAU74767 and AAU74903)

XX Sequence 254 AA;

Query Match

Best Local Similarity 99.6%; Score 1364; DB 5; Length 254;

Matches 253; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATACNPNWFLGYLILVAGSLVSGSCQIINGEDCSPHSQPWQAALVMENELFCSGYL 60

DB 1 MATACNPNWFLGYLILVAGSLVSGSCQIINGEDCSPHSQPWQAALVMENELFCSGYL 60

QY 61 VHPQWLSAAHCFQNSYITIGLHLSLEADQEPGSMVEASLSVRHPEYNRPPLANDLMLI 120

DB 61 VHPQWLSAAHCFQNSYITIGLHLSLEADQEPGSMVEASLSVRHPEYNRPPLANDLMLI 120
QY 121 KLDESVSSESDTIRISISIASOCPAGNSCLVSGWGLLANGRMPTVLOCVNVSVVSEEVCSK 180
DB 121 KLDESVSSESDTIRISISIASOCPAGNSCLVSGWGLLANGRMPTVLOCVNVSVVSEEVCSK 180
QY 181 LYDPLYHPSMFCAGGQDQKDSNGDSGGPLICNGYLQGLVSGKAPCGQGVGVVYTNL 240
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QY 241 CKFTIEWIEKTVQAS 254
DB 241 CKFTIEWIEKTVQAS 254

Search completed: May 5, 2004, 16:07:56

Job time : 62 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2004, 16:09:28 ; Search time 47 Seconds
(without alignments)
1498.003 Million cell updates/sec

Title: US-09-895-814-525

Perfect score: 1369

Sequence: 1 MATAGNPGWFLGYLILGVA.....GVYTLCKFTWIEKTVQAS 254

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1138120 seqs, 277189581 residues

Total number of hits satisfying chosen parameters: 1138120

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
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- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1369	100.0	254	9	US-09-759-143-525
2	1369	100.0	254	9	US-09-780-669-525
3	1369	100.0	254	9	US-09-822-827-525
4	1369	100.0	254	9	US-09-895-793-525
5	1369	100.0	254	9	US-09-895-814-525
6	1369	100.0	254	13	US-10-012-896-525
7	1369	100.0	254	14	US-10-010-940-525
8	1369	100.0	254	14	US-10-144-678A-525
9	1369	100.0	254	14	US-10-294-025-525
10	1369	100.0	1079	9	US-09-822-827-947
11	1369	100.0	1079	9	US-09-895-793-947
12	1364	99.6	254	14	US-10-312-089-525
13	1352	98.8	254	9	US-09-759-143-523
14	1352	98.8	254	9	US-09-780-669-523
15	1352	98.8	254	9	US-09-822-827-523

15	1352	98.8	254	9	US-09-895-793-523	Sequence 523, App
17	1352	98.8	254	9	US-09-895-814-523	Sequence 523, App
18	1352	98.8	254	13	US-10-012-896-523	Sequence 523, App
19	1352	98.8	254	14	US-10-010-940-523	Sequence 523, App
20	1352	98.8	254	14	US-10-144-678A-523	Sequence 523, App
21	1352	98.8	254	14	US-10-294-025-523	Sequence 523, App
22	1348.5	98.5	253	12	US-10-344-394-37	Sequence 37, Appl
23	1205	88.0	449	9	US-09-759-143-617	Sequence 617, App
24	1205	88.0	449	9	US-09-780-669-617	Sequence 617, App
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33	1205	88.0	585	9	US-09-895-793-981	Sequence 978, App
34	1205	88.0	585	9	US-09-895-793-981	Sequence 981, App
35	1205	88.0	585	14	US-10-144-678A-1020	Sequence 1020, App
36	1205	88.0	585	14	US-10-294-025-1020	Sequence 1020, App
37	1205	88.0	801	9	US-09-822-827-982	Sequence 982, App
38	1205	88.0	801	9	US-09-895-793-982	Sequence 982, App
39	1191	87.0	226	14	US-10-312-089-8	Sequence 8, Appli
40	1191	87.0	312	14	US-10-312-089-3	Sequence 3, Appli
41	1191	87.0	344	9	US-09-822-827-973	Sequence 973, App
42	1191	87.0	344	9	US-09-895-793-973	Sequence 973, App
43	1185	86.6	220	9	US-09-759-143-327	Sequence 327, App
44	1185	86.6	220	9	US-09-780-669-327	Sequence 327, App
45	1185	86.6	220	9	US-09-822-827-327	Sequence 327, App

ALIGNMENTS

RESULT 1

US-09-759-143-525
; Sequence 525, Application US/09759143
; Patent No. US2002002248A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun C.
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yiqui
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedwick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 525
LENGTH: 254
TYPE: PRT
ORGANISM: Homo sapien

US-09-759-143-525

Query Match 100.0%; Score 1369; DB 9; Length 254;
Best Local Similarity 100.0%; Pred. No. 4.7e-131;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MATAGNPGWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWOAALVMENELFCSGVL 60
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Db 181 LYDPLYHPSMFCAGGQDQKDCNCGDSGGPLICNGYLQGLVSGKAPCGQVGPVYTNL 240
QY 241 CKFTEWIEKTVQAS 254
Db 241 CKFTEWIEKTVQAS 254

RESULT 2

US-09-780-669-525

; Sequence 525, Application US/09780669

; Patent No. US20020051977A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqui

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hural, John

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Houghton, Raymond L.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.427C24

; CURRENT APPLICATION NUMBER: US/09/780,669

; CURRENT FILING DATE: 2001-02-09

; NUMBER OF SEQ ID NOS: 943

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 525

; LENGTH: 254

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-780-669-525

Query Match 100.0%; Score 1369; DB 9; Length 254;

Best Local Similarity 100.0%; Pred. No. 4.7e-131;

Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Jiang, Yuqui

APPLICANT: Kalos, Michael D.

APPLICANT: Retter, Marc W.

APPLICANT: Stolk, John A.

APPLICANT: Day, Craig H.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Carter, Darrick

APPLICANT: Li, Samuel X.

Db 121 KLDSESVESDTRISISASQCTAGNSCLVSGWGLLANGRMPTVLQCVNVSVSEVCSK 180
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RESULT 3

US-09-822-827-525

; Sequence 525, Application US/09822827

; Patent No. US20020081680A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.534C1

; CURRENT APPLICATION NUMBER: US/09/822,827

; NUMBER OF SEQ ID NOS: 982

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 525

; LENGTH: 254

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-822-827-525

Query Match 100.0%; Score 1369; DB 9; Length 254;

Best Local Similarity 100.0%; Pred. No. 4.7e-131;

Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Jiang, Yuqui

APPLICANT: Kalos, Michael D.

APPLICANT: Retter, Marc W.

APPLICANT: Stolk, John A.

APPLICANT: Day, Craig H.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Carter, Darrick

APPLICANT: Li, Samuel X.

QY 1 MATAGNPGWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWOAALVMENELFCSGVL 60
Db 1 MATAGNPGWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQPWOAALVMENELFCSGVL 60
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Db 121 KLDSESVESDTRISISASQCTAGNSCLVSGWGLLANGRMPTVLQCVNVSVSEVCSK 180
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QY 241 CKFTEWIEKTVQAS 254
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RESULT 4

US-09-895-793-525

; Sequence 525, Application US/09895793

; Publication No. US20020192763A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqui

; APPLICANT: Kalos, Michael D.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel X.

```

; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 525
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-895-793-525

Query Match 100.0%; Score 1369; DB 9; Length 254;
Best Local Similarity 100.0%; Pred. No. 4.7e-131;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 241 CKTEWIEKTVQAS 254

RESULT 5
US-09-895-814-525
; Sequence 525, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriack
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meacher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012.896

; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 525
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-895-814-525

Query Match 100.0%; Score 1369; DB 9; Length 254;
Best Local Similarity 100.0%; Pred. No. 4.7e-131;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6
US-10-012-896-525
; Sequence 525, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriack
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meacher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012.896
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; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 525
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-012-896-525

Query Match      100.0%; Score 1369; DB 13; Length 254;
Best Local Similarity 100.0%; Pred. No. 4.7e-131;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATAGNPGWFLGYLLGVAGSLVSGSCQIINGEDCSPHSQPQWQAALVMENELFCSGVL 60
DB 1 MATAGNPGWFLGYLLGVAGSLVSGSCQIINGEDCSPHSQPQWQAALVMENELFCSGVL 60

QY 61 VHPQWLSAAHCFQNSYITIGLHSLSEADQPGSQMVEASLSVRHPEYNRPPLANDLMLI 120
DB 61 VHPQWLSAAHCFQNSYITIGLHSLSEADQPGSQMVEASLSVRHPEYNRPPLANDLMLI 120

QY 121 KLDSEVSSEDTIRISIASQCPAGNSCLVSGWGLLANGRMPTVLCQVNVSVSEVCSK 180
DB 121 KLDSEVSSEDTIRISIASQCPAGNSCLVSGWGLLANGRMPTVLCQVNVSVSEVCSK 180

QY 121 KLDSEVSSEDTIRISIASQCPAGNSCLVSGWGLLANGRMPTVLCQVNVSVSEVCSK 180
DB 121 KLDSEVSSEDTIRISIASQCPAGNSCLVSGWGLLANGRMPTVLCQVNVSVSEVCSK 180

QY 181 LYDPLXHPMFACAGGQDQKDCNGDSGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
DB 181 LYDPLXHPMFACAGGQDQKDCNGDSGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240

QY 241 CKFTWIEKTVQAS 254
DB 241 CKFTWIEKTVQAS 254

RESULT 7
US-10-010-940-525
; Sequence 525, Application US/10010940
; Publication No. US2003008062A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Stolk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427D3
; CURRENT APPLICATION NUMBER: US/10/010,940
; CURRENT FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 525
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-010-940-525

Query Match      100.0%; Score 1369; DB 14; Length 254;
Best Local Similarity 100.0%; Pred. No. 4.7e-131;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATAGNPGWFLGYLLGVAGSLVSGSCQIINGEDCSPHSQPQWQAALVMENELFCSGVL 60
DB 1 MATAGNPGWFLGYLLGVAGSLVSGSCQIINGEDCSPHSQPQWQAALVMENELFCSGVL 60

QY 61 VHPQWLSAAHCFQNSYITIGLHSLSEADQPGSQMVEASLSVRHPEYNRPPLANDLMLI 120
DB 61 VHPQWLSAAHCFQNSYITIGLHSLSEADQPGSQMVEASLSVRHPEYNRPPLANDLMLI 120

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DB 61 VHPQWLSAAHCFQNSYITIGLHSLSEADQPGSQMVEASLSVRHPEYNRPPLANDLMLI 120
QY 121 KLDSEVSSEDTIRISIASQCPAGNSCLVSGWGLLANGRMPTVLCQVNVSVSEVCSK 180
DB 121 KLDSEVSSEDTIRISIASQCPAGNSCLVSGWGLLANGRMPTVLCQVNVSVSEVCSK 180
QY 181 LYDPLXHPMFACAGGQDQKDCNGDSGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
DB 181 LYDPLXHPMFACAGGQDQKDCNGDSGGPLICNGYLQGLVSGKAPCGQGVPGVYTNL 240
QY 241 CKFTWIEKTVQAS 254
DB 241 CKFTWIEKTVQAS 254

RESULT 8
US-10-144-678A-525
; Sequence 525, Application US/10144678A
; Publication No. US20030157089A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John H.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yaseir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C28
; CURRENT APPLICATION NUMBER: US/10/144,678A
; CURRENT FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 525
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-678A-525

Query Match      100.0%; Score 1369; DB 14; Length 254;
Best Local Similarity 100.0%; Pred. No. 4.7e-131;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MATAGNPGWFLGYLLGVAGSLVSGSCQIINGEDCSPHSQPQWQAALVMENELFCSGVL 60

QY 61 VHPQWLSAAHCFQNSYITIGLHSLSEADQPGSQMVEASLSVRHPEYNRPPLANDLMLI 120
DB 61 VHPQWLSAAHCFQNSYITIGLHSLSEADQPGSQMVEASLSVRHPEYNRPPLANDLMLI 120
QY 121 KLDSEVSSEDTIRISIASQCPAGNSCLVSGWGLLANGRMPTVLCQVNVSVSEVCSK 180
DB 121 KLDSEVSSEDTIRISIASQCPAGNSCLVSGWGLLANGRMPTVLCQVNVSVSEVCSK 180

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; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Repler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780.669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 523
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
; NAME/KEY: VARIANT
; LOCATION: (1)...(254)
; OTHER INFORMATION: Xaa = any amino acid
;
US-09-780-669-523

Query Match      98.8%; Score 1352; DB 9; Length 254;
Best Local Similarity 98.8%; Pred. No. 2.6e-129;
Matches 251; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MATAGNPMGWFLGYLLILGVAGSLVSGSCSIINGEDCSPHSQPQWQAALVMENELFCSGVL 60
Db 1 MATAGNPMGWFLGYLLILGVAGSLVSGSCSIINGEDCSPHSQPQWQAALVMENELFCSGVL 60
Qy 61 VHPQWVLSAAHCFQNSYTIIGLHLSLEADQEPGSMQVEASLSVRHPEYNRPILLANDMLI 120
Db 61 VHPQWVLSATHCFQNSYTIIGLHLSLEADQEPGSMQVEASLSVRHPEYNRPILLANDMLI 120
Qy 121 KLDESVSSEDTRISISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
Db 121 KLDESVSSEDTRISISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
Qy 181 LYDPLYHPSMFCAGGGQXQDSCNGDSGGPLICNGYLQGLVSPGKAPCGQVGPVYTNL 240
Db 181 LYDPLYHPSMFCAGGGQXQDSCNGDSGGPLICNGYLQGLVSPGKAPCGQVGPVYTNL 240
Qy 241 CKFTIEWIEKTVQAS 254
Db 241 CKFTIEWIEKTVQAS 254
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Search completed: May 5, 2004, 16:15:19
Job time : 48 secs

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Query Match      98.8%; Score 1352; DB 9; Length 254;
Best Local Similarity 98.8%; Pred. No. 2.6e-129;
Matches 251; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MATAGNPMGWFLGYLLILGVAGSLVSGSCSIINGEDCSPHSQPQWQAALVMENELFCSGVL 60
Db 1 MATAGNPMGWFLGYLLILGVAGSLVSGSCSIINGEDCSPHSQPQWQAALVMENELFCSGVL 60
Qy 61 VHPQWVLSAAHCFQNSYTIIGLHLSLEADQEPGSMQVEASLSVRHPEYNRPILLANDMLI 120
Db 61 VHPQWVLSATHCFQNSYTIIGLHLSLEADQEPGSMQVEASLSVRHPEYNRPILLANDMLI 120
Qy 121 KLDESVSSEDTRISISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
Db 121 KLDESVSSEDTRISISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
Qy 181 LYDPLYHPSMFCAGGGQXQDSCNGDSGGPLICNGYLQGLVSPGKAPCGQVGPVYTNL 240
Db 181 LYDPLYHPSMFCAGGGQXQDSCNGDSGGPLICNGYLQGLVSPGKAPCGQVGPVYTNL 240
Qy 241 CKFTIEWIEKTVQAS 254
Db 241 CKFTIEWIEKTVQAS 254
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RESULT 15
US-09-822-827-523
; Sequence 523, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822.827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 523
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2004, 16:06:47 ; Search time 23 Seconds
(without alignments)
570.130 Million cell updates/sec

Title: US-09-895-814-525

Perfect score: 1369

Sequence: 1 MATAGNPWGWFLGYLILGVA.....GVYTNLCKTEWIKTVQAS 254

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1369	100.0	254	4	US-09-439-313-525
2	1369	100.0	254	4	US-09-636-215-525
3	1369	100.0	254	4	US-09-685-166A-525
4	1352	98.8	254	4	US-09-439-313-523
5	1352	98.8	254	4	US-09-636-215-523
6	1352	98.8	254	4	US-09-685-166A-523
7	1205	88.0	449	4	US-09-636-215-617
8	1205	88.0	449	4	US-09-685-166A-617
9	1185	86.6	220	4	US-09-439-313-327
10	1185	86.6	220	4	US-09-352-616A-327
11	1185	86.6	220	4	US-09-233-149A-327
12	1185	86.6	220	4	US-09-636-215-327
13	1185	86.6	220	4	US-09-685-166A-327
14	1185	86.6	220	4	US-09-688-489-327
15	1167.5	85.3	284	4	US-09-386-642-54
16	1160	84.7	248	1	US-08-744-026-1
17	1160	84.7	248	1	US-08-102-732-1
18	1160	84.7	248	3	US-09-261-767-1
19	1124	82.1	232	2	US-08-897-340-31
20	1124	82.1	232	3	US-09-252-329-31
21	1070	78.2	205	3	US-09-030-956-176
22	1070	78.2	205	3	US-09-030-956-176
23	1070	78.2	205	4	US-09-439-313-176
24	1070	78.2	205	4	US-09-352-616A-176
25	1070	78.2	205	4	US-09-233-149A-176
26	1070	78.2	205	4	US-09-159-812-176
27	1070	78.2	205	4	US-09-636-215-176

28 1070 78.2 205 4 US-09-685-166A-176 Sequence 176, App
29 1070 78.2 205 4 US-09-115-453-176 Sequence 176, App
30 1070 78.2 205 4 US-09-688-489-176 Sequence 176, App
31 835 61.0 159 3 US-09-020-956-172 Sequence 172, App
32 835 61.0 159 3 US-09-030-607-172 Sequence 172, App
33 835 61.0 159 4 US-09-439-313-172 Sequence 172, App
34 835 61.0 159 4 US-09-352-616A-172 Sequence 172, App
35 835 61.0 159 4 US-09-233-149A-172 Sequence 172, App
36 835 61.0 159 4 US-09-159-812-172 Sequence 172, App
37 835 61.0 159 4 US-09-636-215-172 Sequence 172, App
38 835 61.0 159 4 US-09-685-166A-172 Sequence 172, App
39 835 61.0 159 4 US-09-115-453-172 Sequence 172, App
40 835 61.0 159 4 US-09-688-489-172 Sequence 838, App
41 830 60.6 166 4 US-09-636-215-838 Sequence 838, App
42 830 60.6 166 4 US-09-685-166A-838 Sequence 2, Appli
43 671 49.0 293 4 US-09-509-908-2 Sequence 5522, Ap
44 584.5 42.7 118 4 US-09-621-976-5522 Sequence 1, Appli
45 581 42.4 268 2 US-08-824-874-1

ALIGNMENTS

RESULT 1

US-09-439-313-525
; Sequence 525, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 525
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-439-313-525

Query Match 100.0%; Score 1369; DB 4; Length 254;
Best Local Similarity 100.0%; Pred. No. 2.7e-132; Indels 0; Gaps 0;
Matches 254; Conservative 0; Mismatches 0;
QY 1 MATAGNPWGWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQFQWQAALVMENELFCSGVL 60
Db 1 MATAGNPWGWFLGYLILGVAGSLVSGSCQIINGEDCSPHSQFQWQAALVMENELFCSGVL 60
QY 61 VHPQWLSAAHCFQNSYTTIGLGHLEADQEPGQWVEASLVRHPEYNRPILLANDMLI 120
Db 61 VHPQWLSAAHCFQNSYTTIGLGHLEADQEPGQWVEASLVRHPEYNRPILLANDMLI 120
QY 121 KLDSESVESDITIRISISIASQCFTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
Db 121 KLDSESVESDITIRISISIASQCFTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
QY 181 LYDPLYPHSMFCAGGGQDKSCNGDSGGPLICNGYLOGLVSGKAPCGQGVGYTNL 240
Db 181 LYDPLYPHSMFCAGGGQDKSCNGDSGGPLICNGYLOGLVSGKAPCGQGVGYTNL 240
QY 241 CKFTEWIKTVQAS 254

```

; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 525
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-685-166A-525

Query Match      100.0%; Score 1369; DB 4; Length 254;
Best Local Similarity 100.0%; Pred. No. 2.7e-132; Indels 0; Gaps 0;
Matches 254; Conservative 0; Mismatches 0;

QY 1 MATAGNPGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPWOAALVMENELFCSGVL 60
DB 1 MATAGNPGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPWOAALVMENELFCSGVL 60

QY 61 VHPQWVLSAAHCFQNSYITIGLHSLADQEPGQWVEASLSVRHPEYNRPLLANDLMLI 120
DB 61 VHPQWVLSAAHCFQNSYITIGLHSLADQEPGQWVEASLSVRHPEYNRPLLANDLMLI 120

QY 121 KLDSESVESDITRSISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
DB 121 KLDSESVESDITRSISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180

QY 181 LYDPLYHPSMFCAGGQDQKSCNGDSGGPLICNGYLGSLVFGKAPCGQGVGVYTNL 240
DB 181 LYDPLYHPSMFCAGGQDQKSCNGDSGGPLICNGYLGSLVFGKAPCGQGVGVYTNL 240

QY 241 CKFTEWIEKTVQAS 254
DB 241 CKFTEWIEKTVQAS 254

RESULT 4
US-09-439-313-523
; Sequence 523, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575

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; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 525
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-636-215-525

Query Match      100.0%; Score 1369; DB 4; Length 254;
Best Local Similarity 100.0%; Pred. No. 2.7e-132; Indels 0; Gaps 0;
Matches 254; Conservative 0; Mismatches 0;

QY 1 MATAGNPGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPWOAALVMENELFCSGVL 60
DB 1 MATAGNPGWFLGYLILGVAGSLVSGSCSQIINGEDCSPHSQPWOAALVMENELFCSGVL 60

QY 61 VHPQWVLSAAHCFQNSYITIGLHSLADQEPGQWVEASLSVRHPEYNRPLLANDLMLI 120
DB 61 VHPQWVLSAAHCFQNSYITIGLHSLADQEPGQWVEASLSVRHPEYNRPLLANDLMLI 120

QY 121 KLDSESVESDITRSISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
DB 121 KLDSESVESDITRSISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180

QY 181 LYDPLYHPSMFCAGGQDQKSCNGDSGGPLICNGYLGSLVFGKAPCGQGVGVYTNL 240
DB 181 LYDPLYHPSMFCAGGQDQKSCNGDSGGPLICNGYLGSLVFGKAPCGQGVGVYTNL 240

QY 241 CKFTEWIEKTVQAS 254
DB 241 CKFTEWIEKTVQAS 254

RESULT 3
US-09-685-166A-525
; Sequence 525, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.

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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 523
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
; NAME/KEY: VARIANT
; LOCATION: (1)...(254)
; OTHER INFORMATION: Xaa = Any amino acid
US-09-439-313-523

Query Match          98.8%; Score 1352; DB 4; Length 254;
Best Local Similarity 98.8%; Pred. No. 1.5e-130;
Matches 251; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MATAGNPGWFLGYLLILGVAGSLVSGSCSIINGEDCSPHSQPWQAALVMENELFCSGVL 60
DB 1 MATAGNPGWFLGYLLILGVAGSLVSGSCSIINGEDCSPHSQPWQAALVMENELFCSGVL 60
QY 61 VHPQWLAAHCFQNSYITIGLHSLADQBPQSQWVEASLSVRHPEYNRPPLANDLMLI 120
DB 61 VHPQWLAAHCFQNSYITIGLHSLADQBPQSQWVEASLSVRHPEYNRPPLANDLMLI 120
QY 121 KLDSEVSSEDTIRISIASQCPAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
DB 121 KLDSEVSSEDTIRISIASQCPAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
QY 181 LYDPLHPSMFCAGGQDQKDCNCGDSGGPLICNGYLQGLVSGFKAPCGQGVPGVYTNL 240
DB 181 LYDPLHPSMFCAGGQDQKDCNCGDSGGPLICNGYLQGLVSGFKAPCGQGVPGVYTNL 240
QY 241 CKFTEWIEKTVQAS 254
DB 241 CKFTEWIEKTVQAS 254

RESULT 5
US-09-636-215-523
; Sequence 523, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 523
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
; NAME/KEY: VARIANT
; LOCATION: (1)...(254)
; OTHER INFORMATION: Xaa = Any amino acid
US-09-685-166A-523

Query Match          98.8%; Score 1352; DB 4; Length 254;
Best Local Similarity 98.8%; Pred. No. 1.5e-130;
Matches 251; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MATAGNPGWFLGYLLILGVAGSLVSGSCSIINGEDCSPHSQPWQAALVMENELFCSGVL 60
DB 1 MATAGNPGWFLGYLLILGVAGSLVSGSCSIINGEDCSPHSQPWQAALVMENELFCSGVL 60
QY 61 VHPQWLAAHCFQNSYITIGLHSLADQBPQSQWVEASLSVRHPEYNRPPLANDLMLI 120
DB 61 VHPQWLAAHCFQNSYITIGLHSLADQBPQSQWVEASLSVRHPEYNRPPLANDLMLI 120
QY 121 KLDSEVSSEDTIRISIASQCPAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
DB 121 KLDSEVSSEDTIRISIASQCPAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEVCSK 180
QY 181 LYDPLHPSMFCAGGQDQKDCNCGDSGGPLICNGYLQGLVSGFKAPCGQGVPGVYTNL 240
DB 181 LYDPLHPSMFCAGGQDQKDCNCGDSGGPLICNGYLQGLVSGFKAPCGQGVPGVYTNL 240
QY 241 CKFTEWIEKTVQAS 254
DB 241 CKFTEWIEKTVQAS 254

RESULT 6
US-09-685-166A-523
; Sequence 523, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 523
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
; NAME/KEY: VARIANT
; LOCATION: (1)...(254)
; OTHER INFORMATION: Xaa = any amino acid
US-09-685-166A-523

Query Match          98.8%; Score 1352; DB 4; Length 254;
Best Local Similarity 98.8%; Pred. No. 1.5e-130;
Matches 251; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 1 MATAGNPGWFLGYLILGAGSLVSGSCSIINGEDCSFHSQPWQAALVMENELFCSGVL 60
DB 1 MATAGNPGWFLGYLILGAGSLVSGSCSIINGEDCSFHSQPWQAALVMENELFCSGVL 60
QY 61 VHPQWVLSAAHCFQNSYTIIGLHSLADQPPGSMQVEASLSVRHPEYNRPILLANDMLI 120
DB 61 VHPQWVLSAAHCFQNSYTIIGLHSLADQPPGSMQVEASLSVRHPEYNRPILLANDMLI 120
QY 121 KLDESVSSEDTRISISIAOQPTAGNSCLVSGWGLLANGRPMTVLQCVNVSVSEVCSK 180
DB 121 KLDESVSSEDTRISISIAOQPTAGNSCLVSGWGLLANGRPMTVLQCVNVSVSEVCSK 180
QY 181 LVDPVLPYHPSMFCAGGQDQKSCNDSGGPLICNGYLQGLVSFGKAPCGQGVGVGYTNL 240
DB 181 LVDPVLPYHPSMFCAGGQDQKSCNDSGGPLICNGYLQGLVSFGKAPCGQGVGVGYTNL 240
QY 241 CKFTWIEKTVOAS 254
DB 241 CKFTWIEKTVOAS 254

RESULT 7
US-09-636-215-617
; Sequence 617, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 617
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-636-215-617

Query Match 88.0%; Score 1205; DB 4; Length 449;
Best Local Similarity 100.0%; Pred. No. 4e-115;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 31 IINGEDCSPHSQPWQAALVMENELFCSGVLVHPQWVLSAAHCFQNSYTIIGLHSLADQ 90
DB 8 IINGEDCSPHSQPWQAALVMENELFCSGVLVHPQWVLSAAHCFQNSYTIIGLHSLADQ 67
QY 91 EPGSQMVEASLSVRHPEYNRPILLANDMLIKLDESVSSEDTRISISIAOQPTAGNSCLV 150
DB 68 EPGSQMVEASLSVRHPEYNRPILLANDMLIKLDESVSSEDTRISISIAOQPTAGNSCLV 127
QY 151 SGWGLLANGRPMTVLQCVNVSVSEVCSKLYDPLVHPMSMFCAGGQDQKSCNDSGGP 210
DB 128 SGWGLLANGRPMTVLQCVNVSVSEVCSKLYDPLVHPMSMFCAGGQDQKSCNDSGGP 187
QY 211 LICNGYLQGLVSFGKAPCGQGVGVGYTNLCKFTWIEKTVOAS 254

DB 188 LICNGYLQGLVSFGKAPCGQGVGVGYTNLCKFTWIEKTVOAS 231
RESULT 8
US-09-685-166A-617
; Sequence 617, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 617
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-685-166A-617

Query Match 88.0%; Score 1205; DB 4; Length 449;
Best Local Similarity 100.0%; Pred. No. 4e-115;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 31 IINGEDCSPHSQPWQAALVMENELFCSGVLVHPQWVLSAAHCFQNSYTIIGLHSLADQ 90
DB 8 IINGEDCSPHSQPWQAALVMENELFCSGVLVHPQWVLSAAHCFQNSYTIIGLHSLADQ 67
QY 91 EPGSQMVEASLSVRHPEYNRPILLANDMLIKLDESVSSEDTRISISIAOQPTAGNSCLV 150
DB 68 EPGSQMVEASLSVRHPEYNRPILLANDMLIKLDESVSSEDTRISISIAOQPTAGNSCLV 127
QY 151 SGWGLLANGRPMTVLQCVNVSVSEVCSKLYDPLVHPMSMFCAGGQDQKSCNDSGGP 210
DB 128 SGWGLLANGRPMTVLQCVNVSVSEVCSKLYDPLVHPMSMFCAGGQDQKSCNDSGGP 187
QY 211 LICNGYLQGLVSFGKAPCGQGVGVGYTNLCKFTWIEKTVOAS 254
DB 188 LICNGYLQGLVSFGKAPCGQGVGVGYTNLCKFTWIEKTVOAS 231

RESULT 9
US-09-439-313-327
; Sequence 327, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary

```
/ APPLICANT: Retter, Mark
/ APPLICANT: Soik, John
/ APPLICANT: Day, Craig
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
/ TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
/ FILE REFERENCE: 210121.427C9
/ CURRENT APPLICATION NUMBER: US/09/439,313
/ CURRENT FILING DATE: 1999-11-12
/ NUMBER OF SEQ ID NOS: 575
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 327
/ LENGTH: 220
/ TYPE: PRT
/ ORGANISM: Homo sapien
US-09-439-313-327

Query Match      86.6%; Score 1185; DB 4; Length 220;
Best Local Similarity 100.0%; Pred. No. 1.6e-113;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 EDCSPHSQPWQAALVMENELFCGVLVHPQWVLSAAHCFQNSYTTIGLHLSLEADQEPGS 94
DB 1 EDCSPHSQPWQAALVMENELFCGVLVHPQWVLSAAHCFQNSYTTIGLHLSLEADQEPGS 60
QY 95 QMVEASLSVRHPEYRNPRLANDMLIKLDESSESDDTIRSIASQCPAGNSCLVSGWG 154
DB 61 QMVEASLSVRHPEYRNPRLANDMLIKLDESSESDDTIRSIASQCPAGNSCLVSGWG 120
QY 155 LLANGRMPTVLCQNVSVVSEVCSKLYDPLVHPMSMFCAGGQDQKDCSNGSGGPLICN 214
DB 121 LLANGRMPTVLCQNVSVVSEVCSKLYDPLVHPMSMFCAGGQDQKDCSNGSGGPLICN 180
QY 215 GYLQGLVSGKAPCGQGVPGVYTNLCKFTWIEKTVQAS 254
DB 181 GYLQGLVSGKAPCGQGVPGVYTNLCKFTWIEKTVQAS 220

RESULT 10
US-09-352-616A-327
/ Sequence 327, Application US/09352616A
/ Patent No. 6395278
/ GENERAL INFORMATION:
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Harlocker, Susan Louise
/ APPLICANT: Jiang, Yuqi
/ APPLICANT: Xu, Jiaqichun
/ APPLICANT: Mitcham, Jennifer Lynn
/ TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
/ TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
/ FILE REFERENCE: 210121.427C8
/ CURRENT APPLICATION NUMBER: US/09/352,616A
/ CURRENT FILING DATE: 1999-07-13
/ NUMBER OF SEQ ID NOS: 472
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 327
/ LENGTH: 220
/ TYPE: PRT
/ ORGANISM: Homo sapien
US-09-352-616A-327

Query Match      86.6%; Score 1185; DB 4; Length 220;
Best Local Similarity 100.0%; Pred. No. 1.6e-113;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 EDCSPHSQPWQAALVMENELFCGVLVHPQWVLSAAHCFQNSYTTIGLHLSLEADQEPGS 94
DB 1 EDCSPHSQPWQAALVMENELFCGVLVHPQWVLSAAHCFQNSYTTIGLHLSLEADQEPGS 60
QY 95 QMVEASLSVRHPEYRNPRLANDMLIKLDESSESDDTIRSIASQCPAGNSCLVSGWG 154
DB 61 QMVEASLSVRHPEYRNPRLANDMLIKLDESSESDDTIRSIASQCPAGNSCLVSGWG 120
QY 155 LLANGRMPTVLCQNVSVVSEVCSKLYDPLVHPMSMFCAGGQDQKDCSNGSGGPLICN 214
DB 121 LLANGRMPTVLCQNVSVVSEVCSKLYDPLVHPMSMFCAGGQDQKDCSNGSGGPLICN 180
QY 215 GYLQGLVSGKAPCGQGVPGVYTNLCKFTWIEKTVQAS 254
DB 181 GYLQGLVSGKAPCGQGVPGVYTNLCKFTWIEKTVQAS 220

RESULT 11
US-09-232-149A-327
/ Sequence 327, Application US/09232149A
/ Patent No. 6465611
/ GENERAL INFORMATION:
/ APPLICANT: Xu, Jiaqichun
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Mitcham, Jennifer Lynn
/ TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
/ TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
/ FILE REFERENCE: 210121.427C6
/ CURRENT APPLICATION NUMBER: US/09/232,149A
/ CURRENT FILING DATE: 1999-01-15
/ NUMBER OF SEQ ID NOS: 338
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 327
/ LENGTH: 220
/ TYPE: PRT
/ ORGANISM: Homo sapien
US-09-232-149A-327

Query Match      86.6%; Score 1185; DB 4; Length 220;
Best Local Similarity 100.0%; Pred. No. 1.6e-113;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 EDCSPHSQPWQAALVMENELFCGVLVHPQWVLSAAHCFQNSYTTIGLHLSLEADQEPGS 94
DB 1 EDCSPHSQPWQAALVMENELFCGVLVHPQWVLSAAHCFQNSYTTIGLHLSLEADQEPGS 60
QY 95 QMVEASLSVRHPEYRNPRLANDMLIKLDESSESDDTIRSIASQCPAGNSCLVSGWG 154
DB 61 QMVEASLSVRHPEYRNPRLANDMLIKLDESSESDDTIRSIASQCPAGNSCLVSGWG 120
QY 155 LLANGRMPTVLCQNVSVVSEVCSKLYDPLVHPMSMFCAGGQDQKDCSNGSGGPLICN 214
DB 121 LLANGRMPTVLCQNVSVVSEVCSKLYDPLVHPMSMFCAGGQDQKDCSNGSGGPLICN 180
QY 215 GYLQGLVSGKAPCGQGVPGVYTNLCKFTWIEKTVQAS 254
DB 181 GYLQGLVSGKAPCGQGVPGVYTNLCKFTWIEKTVQAS 220

RESULT 12
US-09-636-215-327
/ Sequence 327, Application US/09636215
/ Patent No. 6620922
/ GENERAL INFORMATION:
/ APPLICANT: Xu, Jiaqichun
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Mitcham, Jennifer L.
/ APPLICANT: Harlocker, Susan L.
/ APPLICANT: Jiang, Yuqi
/ APPLICANT: Henderson, Robert A.
/ APPLICANT: Kalos, Michael D.
/ APPLICANT: Fanger, Gary R.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Stolk, John A.
/ APPLICANT: Day, Craig H.
/ APPLICANT: Vecvick, Thomas S.
/ APPLICANT: Carter, Darrick
/ APPLICANT: Li, Samuel
/ APPLICANT: Wang, Aijun
/ APPLICANT: Skeiky, Yasar A.W.
/ APPLICANT: Hepler, William
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
```

;; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
;; FILE REFERENCE: 210121.42717C17
;; CURRENT APPLICATION NUMBER: US/09/636,215
;; CURRENT FILING DATE: 2000-08-10
;; NUMBER OF SEQ ID NOS: 852
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 327
;; LENGTH: 220
;; TYPE: PR1
;; ORGANISM: Homo sapien
US-09-636-215-327

Query Match 86.6%; Score 1185; DB 4; Length 220;
Best Local Similarity 100.0%; Pred. No. 1.6e-113;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 35 EDCSPHSQWQAALVWENELFCGVLVHPQWLSAAHCFQNSYTIIGLHLSLEADQEPGS 94
Db 1 EDCSPHSQWQAALVWENELFCGVLVHPQWLSAAHCFQNSYTIIGLHLSLEADQEPGS 60
QY 95 QMVEASLSVRHPEYRNPRLANDMLIKLDESVSSEDTIRSIASQCTAGNSCLVSGWG 154
Db 61 QMVEASLSVRHPEYRNPRLANDMLIKLDESVSSEDTIRSIASQCTAGNSCLVSGWG 120
QY 155 LLANGRMPTVLOCNVSVVSEVCSKLYDPLVHPMSFCAAGGQDQKDCNCGDSGGPLCN 214
Db 121 LLANGRMPTVLOCNVSVVSEVCSKLYDPLVHPMSFCAAGGQDQKDCNCGDSGGPLCN 180
QY 215 GYLOGLVSFGKAPCGQGVPGVYTNLCFTETWIEKTVQAS 254
Db 181 GYLOGLVSFGKAPCGQGVPGVYTNLCFTETWIEKTVQAS 220

RESULT 13
US-09-685-166A-327
; Sequence 327, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 327
; LENGTH: 220
; TYPE: PR1
; ORGANISM: Homo sapien
US-09-685-166A-327

Query Match 86.6%; Score 1185; DB 4; Length 220;
Best Local Similarity 100.0%; Pred. No. 1.6e-113;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 35 EDCSPHSQWQAALVWENELFCGVLVHPQWLSAAHCFQNSYTIIGLHLSLEADQEPGS 94

Db 1 EDCSPHSQWQAALVWENELFCGVLVHPQWLSAAHCFQNSYTIIGLHLSLEADQEPGS 60
QY 95 QMVEASLSVRHPEYRNPRLANDMLIKLDESVSSEDTIRSIASQCTAGNSCLVSGWG 154
Db 61 QMVEASLSVRHPEYRNPRLANDMLIKLDESVSSEDTIRSIASQCTAGNSCLVSGWG 120
QY 155 LLANGRMPTVLOCNVSVVSEVCSKLYDPLVHPMSFCAAGGQDQKDCNCGDSGGPLCN 214
Db 121 LLANGRMPTVLOCNVSVVSEVCSKLYDPLVHPMSFCAAGGQDQKDCNCGDSGGPLCN 180
QY 215 GYLOGLVSFGKAPCGQGVPGVYTNLCFTETWIEKTVQAS 254
Db 181 GYLOGLVSFGKAPCGQGVPGVYTNLCFTETWIEKTVQAS 220

RESULT 14
US-09-688-489-327
; Sequence 327, Application US/09688489
; Patent No. 6664377
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; FILE REFERENCE: 210121.427D2
; CURRENT APPLICATION NUMBER: US/09/688,489
; CURRENT FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 327
; LENGTH: 220
; TYPE: PR1
; ORGANISM: Homo sapien
US-09-688-489-327

Query Match 86.8%; Score 1185; DB 4; Length 220;
Best Local Similarity 100.0%; Pred. No. 1.6e-113;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 35 EDCSPHSQWQAALVWENELFCGVLVHPQWLSAAHCFQNSYTIIGLHLSLEADQEPGS 94
Db 1 EDCSPHSQWQAALVWENELFCGVLVHPQWLSAAHCFQNSYTIIGLHLSLEADQEPGS 60
QY 95 QMVEASLSVRHPEYRNPRLANDMLIKLDESVSSEDTIRSIASQCTAGNSCLVSGWG 154
Db 61 QMVEASLSVRHPEYRNPRLANDMLIKLDESVSSEDTIRSIASQCTAGNSCLVSGWG 120
QY 155 LLANGRMPTVLOCNVSVVSEVCSKLYDPLVHPMSFCAAGGQDQKDCNCGDSGGPLCN 214
Db 121 LLANGRMPTVLOCNVSVVSEVCSKLYDPLVHPMSFCAAGGQDQKDCNCGDSGGPLCN 180
QY 215 GYLOGLVSFGKAPCGQGVPGVYTNLCFTETWIEKTVQAS 254
Db 181 GYLOGLVSFGKAPCGQGVPGVYTNLCFTETWIEKTVQAS 220

RESULT 15
US-09-386-642-54
; Sequence 54, Application US/09386642
; Patent No. 6420157
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jensen
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: ORT-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 54

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; LENGTH: 284
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Human MH2
; OTHER INFORMATION: protease in PFEK zymogen vector
US-09-386-642-54

Query Match      85.3%; Score 1167.5; DB 4; Length 284;
Best Local Similarity 96.5%; Pred. No. 1.5e-111;
Matches 218; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 30 QIINGEDC-SPHSQPWQAALVWENELFCSGVLVHPQWVLSAAHCFQNSYTIGLGHSLEA 88
Db 51 KIVGGYNCLPHSQPWQAALVWENELFCSGVLVHPQWVLSAAHCFQNSYTIGLGHSLEA 110
QY 89 DQEPGQWVEASLSVRHPEYNRPILLANDMLIKLDESVSBSDTIRISISIAQCPTAGNSC 148
Db 111 DQEPGQWVEASLSVRHPEYNRPILLANDMLIKLDESVSBSDTIRISISIAQCPTAGNSC 170
QY 149 LVSGMGLLANGRMPTVLQCVNVSVVSEEVCSKLYDPLYHPSMFCAAGGQDQKDCNGDSG 208
Db 171 LVSGMGLLANGRMPTVLQCVNVSVVSEEVCSKLYDPLYHPSMFCAAGGQDQKDCNGDSG 230
QY 209 GPLICNGYLGIVSFGKAPCCQGVPGVYTNLCKFTWIEKTVQAS 254
Db 231 GPLICNGYLGIVSFGKAPCCQGVPGVYTNLCKFTWIEKTVQAS 276
```

Search completed: May 5, 2004, 16:10:31
Job time : 24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 5, 2004, 16:04:47 ; Search time 20 seconds
(without alignments)
1221.632 Million cell updates/sec

Title: US-09-895-814-525

Perfect score: 1369

Sequence: 1 MATAGNFWGFLGYLILGVA.....GVYTNLCKFTWIKTVQAS 254

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 781*

1: Pirl.*

2: Pirl2.*

3: Pirl3.*

4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	567.5	41.5	253	2 A53968	serine proteinase
2	563.5	41.2	260	2 I56559	neuropsin - mouse
3	524	38.3	261	2 A45303	tissue kallikrein
4	515	37.6	244	2 A44284	tissue kallikrein
5	510.5	37.3	248	2 S55066	trypsin (EC 3.4.21
6	509	37.2	261	1 NGMSG	7S nerve growth fa
7	507	37.0	261	2 A34079	tissue kallikrein
8	506	37.0	247	2 A27547	trypsin (EC 3.4.21
9	506	37.0	261	2 S01971	tissue kallikrein
10	503	36.7	261	2 J02336	tissue kallikrein
11	503	36.7	261	2 A31136	tissue kallikrein
12	502.5	36.7	246	2 J01472	trypsin (EC 3.4.21
13	502.5	36.7	261	2 A29586	tissue kallikrein
14	502	36.7	261	2 A41020	tissue kallikrein
15	501.5	36.6	250	2 T01779	trypsin (EC 3.4.21
16	499.5	36.5	246	1 TRDGC	trypsin (EC 3.4.21
17	498	36.4	261	1 A32297	semenogelase (EC 3
18	497	36.3	247	2 S05494	trypsin (EC 3.4.21
19	497	36.3	259	2 B31136	tissue kallikrein
20	496	36.2	248	2 S55067	trypsin (EC 3.4.21
21	496	36.2	258	2 A29746	tissue kallikrein
22	496	36.2	265	1 K0RTP	tissue kallikrein
23	495.5	36.2	246	2 J01471	trypsin (EC 3.4.21
24	492.5	36.0	261	2 A29745	tissue kallikrein
25	492	35.9	257	2 S33772	tissue kallikrein
26	491	35.9	261	1 EGMSB	tissue kallikrein
27	488.5	35.7	261	1 A25606	tissue kallikrein
28	487.5	35.6	262	1 K0HU	tissue kallikrein
29	485	35.4	246	1 TRRT1	trypsin (EC 3.4.21

30 485 35.4 261 1 S35711 semenogelase (EC 3
31 484 35.4 259 1 K0RTTN tonin (EC 3.4.21.-
32 484 35.4 261 1 TRMSMS tissue kallikrein
33 480 35.1 247 2 S13813 trypsin (EC 3.4.21
34 480 35.1 261 1 K0MS1 tissue kallikrein
35 479.5 35.0 229 1 TRBOTR trypsin (EC 3.4.21
36 479 35.0 246 2 B25528 trypsin (EC 3.4.21
37 476.5 34.8 242 2 S49489 trypsin (EC 3.4.21
38 472.5 34.5 231 1 TRPGTR trypsin (EC 3.4.21
39 472.5 34.5 247 1 TRDG trypsin (EC 3.4.21
40 471 34.4 259 2 D23863 tissue kallikrein
41 470.5 34.4 263 2 S15686 tissue kallikrein
42 470 34.3 243 2 A35871 trypsin (EC 3.4.21
43 469.5 34.3 260 2 A37938 tissue kallikrein
44 467.5 34.1 238 2 S31779 trypsin (EC 3.4.21
45 467.5 34.1 247 1 A25852 trypsin (EC 3.4.21

ALIGNMENTS

RESULT 1

A53968

serine proteinase SCCE precursor - human

N/Alternate names: stratum corneum chymotryptic enzyme

C/Species: Homo sapiens (man)

C/Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 22-Jun-1999

C/Accession: A53968

R/Hansson, L.; Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T.

J. Biol. Chem. 269, 19420-19426, 1994

A/Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzym

A/Reference number: A53968; MUID:94308225; PMID:8034709

A/Accession: A53968

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-253 <HAN>

A/Cross-references: GB:L33404; NID:G521214; PIDN:AAC37551.1; PID:G532504

C/Genetics:

A/Genes: GDB:PRSS6; SCCE

A/Cross-references: GDB:377730

A/Map position: 7q35-7q35

C/Superfamily: trypsin; trypsin homology

F:30-245/Domain: trypsin homology <TRY>

Query Match 41.5%; Score 567.5; DB 2; Length 253;
Best Local Similarity 46.2%; Pred. No. 5.6e-42;
Matches 111; Conservative 40; Mismatches 82; Indels 7; Gaps 4;
QY 15 LILGVAGSLVSGSCQIINGEDCSPHSQPQWQALVWNEIFCSGVLVHPQWVLSAHCQFQ 74
Db 16 LALETAGEAQ--DKIIDGAPCARGSHPWQVALLSGNQLHCGGVLVNRWVLTAAHCKM 73
QY 75 NSYITGLIHSLDADQEPGQSMVEASLSVRHPEYNRPILLANDMLIKLDESVSSEDTIRS 134
Db 74 NEYTHLGSDTL-GDPR--AQRIKASKFRHPGYSTQTHVNDMLVKNLQARLSMWVK 130
QY 135 ISIASQCTPAGNSCLVSGWGLANG--RMPTVLQCNVSVVSEEVCSKLYDPLIYHPSMPC 192
Db 131 VRLPSRCEPPGTCTVSGNGTTTSPDVTFFPSDLNMCVDVKLISPQDCTKYKDLLENSMLC 190
QY 193 AGGGQDKDSNGSDGGPLICNGYLGVSFQKPGQGVGVVTNLCKFTWIKTVQ 252
Db 191 AGIPDSKNACNGSDGGPLVCRGTLQGLVSWGTFFCGQPNDFGVITQVCKFTKWNIDTWK 250

RESULT 2

I56559

neuropsin - mouse

C/Species: Mus musculus (house mouse)

C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000

C/Accession: I56559

R/Chen, Z.L.; Yoshida, S.; Kato, K.; Momota, Y.; Suzuki, J.; Tanaka, T.; Ito, J.; Nishin

J. Neurosci. 15, 5088-5097, 1995

A>Title: Expression and activity-dependent changes of a novel limbic-serine protease gene
 A:Reference number: 156559; MUID:95348817; PMID:7623137
 A:Accession: I56559
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-260 <RES>
 A:Cross-references: GB:D30785; NID:g1648847; PIDN:BAA06451.1; PID:g1020091
 C:Superfamily: trypsin; trypsin homology
 F:33-252/Domain: trypsin homology <TRY>

Query Match 41.2%; Score 563.5; DB 2; Length 260;
 Best Local Similarity 41.3%; Pred. No. 1.3e-41;
 Matches 102; Conservative 47; Mismatches 91; Indels 7; Gaps 4;

QY 10 WFLGVLILGVAGSLVSGSCSIINGEDCSPHSQPQWALVWENELFCGVLVHPQWLSA 69
 DB 12 WILLFLFWAGLFRAGSLKLEKRECIQSPQWALVWENELFCGVLVGRWVITA 71
 QY 70 AHCFQNSYITGLHSLLEADQEPGQWVEASLVSRHPEYRPL---LANDMLIKLDES 126
 DB 72 ARCKKQKYSVRLGDHSLQSRQP-EQEIQAQSIQHPCYNNSPEDHSHDMLRLQNSA 130
 QY 127 SESPTIRISIASQCPPTAGNSCLVSGGALLANGR--NPTVLQCVNVSVSEVCSKLYDP 184
 DB 131 NLGDKKVPQVLANLCKFKYQCKIISGWTGTVSPQENFNTLCAEVKIYSONKCEAYPG 190
 QY 185 LYHPSMFCAGGQDQKDCSNGDSGGLPCNGYLQGLVSGFKAPCGQVGPVYTNLCKFT 244
 DB 191 KITEGMVCA-GSSNGADTCQDGGGFLVCDGVLQGIISWGSDDPGCKEKGVTIKICRYT 249
 QY 245 EWIEKTV 251
 DB 250 TWIKETM 256

RESULT 3
 S45303
 tissue kallikrein (EC 3.4.21.35) precursor - dog
 C:Species: Canis lupus familiaris (dog)
 C:Date: 20-Oct-1994 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999
 C:Accession: S45303; S38487
 R:Gauthier, E.R.; Dumas, C.; Chapdelain, P.; Tremblay, R.R.; Dube, J.Y.
 Biochim. Biophys. Acta 1218, 102-104, 1994
 A>Title: Characterization of canine pancreas kallikrein cDNA.
 A:Reference number: S45303; MUID:94250683; PMID:8193155
 A:Accession: S45303
 A:Molecule type: mRNA
 A:Residues: 1-261 <GAU>
 A:Cross-references: EMBL:X75479; NID:9414018; PIDN:CAA53210.1; PID:g414019
 C:Superfamily: trypsin; trypsin homology
 C:Keywords: hydrolase; serine proteinase
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-261/Product: tissue kallikrein #status predicted <MAT>
 F:25-253/Domain: trypsin homology <TRY>
 F:65,120,213/Active site: His, Asp, Ser #status predicted

Query Match 38.3%; Score 524; DB 2; Length 261;
 Best Local Similarity 40.3%; Pred. No. 3.6e-38;
 Matches 106; Conservative 51; Mismatches 84; Indels 22; Gaps 6;

QY 10 WFLGY-LILGVAGSLVSGSC---SQIINGEDCSPHSQPQWALVWENELFCGVLVHPQ 64
 DB 2 WFLVLCIALSLAG---TGAAPVQSRIGWDCIKNSQPWQALYHYSKFCQCGVLVHPE 58
 QY 65 WLSNAHCFQNSYITGLHSLLEADQEPGQWVEASLVSRHPEYRPLAN-----115
 DB 59 WYVTAACHINDYNQWLGRYNL-FEHEDTAQVQVRSFPHPEFNLKLNHRTLPBEDY 117
 QY 116 --DLMLIKLDESVDSTIRISIASQCPPTAGNSCLVSGGALLANGRM--PTVLQCVNV 171
 DB 118 SHDINLLRLAEPAQITDAVRLDLPTQEPQVGSICYSAGWSGIPEFDKFIYDDDLQCVDLE 177
 QY 172 VVSEVCSKLYDPLVHPSMFCAGGQDQKDCSNGDSGGLPCNGYLQGLVSGFKAPCGQV 231

Db 178 LISNDICANAHSQKVTFFMLCAHGLEGGKDTCTGSGGGLICDGLVQGITSMGHVPCGSP 237
 QY 232 GVGVTYNLCKFTETWIEKTVQAS 254
 Db 238 NMPAVYTKVISHLEWIKETMTAN 260

RESULT 4
 A44284
 tissue kallikrein (EC 3.4.21.35) homolog - rat (fragment)
 N:Alternate names: proteinase B light chain
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 22-Jun-1999
 C:Accession: A44284; C41429
 R:Ma, J.X.; Chao, J.; Chao, L.
 Biochemistry 31, 10922-10928, 1992
 A>Title: Molecular cloning and characterization of rKlk10, a cDNA encoding T-kinogenase
 A:Reference number: A44284; MUID:93041794; PMID:1420203
 A:Accession: A44284
 A:Molecule type: nucleic acid
 A:Residues: 1-244 <MAL>
 A:Cross-references: GB:S48142; NID:g259430; PIDN:AAB24071.1; PID:g259431
 A:Experimental source: submandibular gland
 A>Note: sequence extracted from NCBI backbone (NCBI:118095, NCBI:118096)
 R:Kato, H.; Nakanishi, E.; Enjiyoji, K.; Hayashi, S.; Iwanaga, S.
 J. Biochem. 102, 1389-1404, 1987
 A>Title: Characterization of serine proteinases isolated from rat submaxillary gland: wi
 A:Reference number: A41429; MUID:86198057; PMID:3482210
 A:Accession: C41429
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 10-61 <KAT>
 C:Superfamily: trypsin; trypsin homology
 C:Keywords: hydrolase; serine proteinase
 F:10-236/Domain: trypsin homology <TRY>
 F:48,103,196/Active site: His, Asp, Ser #status predicted

Query Match 37.6%; Score 515; DB 2; Length 244;
 Best Local Similarity 42.4%; Pred. No. 2e-37;
 Matches 101; Conservative 42; Mismatches 77; Indels 19; Gaps 5;

QY 29 SQIINGEDCSPHSQPQWALVWENELFCGVLVHPQWLSAHCFCQNSYITGLHSLSEA 88
 DB 8 SRIVGGYCKEKNSQPWQVAIL--NEYLCGGVLIDPSWVITAAHCYSNYHYVLLGRNNLFE 65
 QY 89 DOBPQSQWVEASLVSRHPEYRPL-----ANDMLIKLDESVDSTIRIS 136
 DB 66 D-EPAQYRFVQNSPPHEDY-KPFLMRNHTQRGDDYSNDLMLHLEPADITDGKVID 123
 QY 137 IASQPTAGNSCLVSGWGLL--ANGRMPTVLQCVNVSVSEVCSKLYDPLVHPSMFCAG 194
 DB 124 LPTEEPKVGSTCLASGWSGSKPLANWELPDDLQCVNIHLLSNEKCTEAYEQKVTDLMLCAG 183
 QY 195 GGQDQKDCSNGDSGGLPCNGYLQGLVSGFKAPCGQVGPVYTNLCKFTETWIEKTVQ 252
 DB 184 EMDGRKDTCKGSGGGLICDGLVQGITSMGHVPCAEYPNPGVYTKLIFTSWIKVMK 241

RESULT 5
 S55066
 trypsin (EC 3.4.21.4) II precursor, pancreatic (clone 2-P29) - chicken
 N:Alternate names: trypsinogen II
 C:Species: Gallus gallus (chicken)
 C:Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 22-Jun-1999
 C:Accession: S55066; S72347
 R:Wang, K.; Gan, L.; Lee, I.; Hood, L.
 Biochem. J. 307, 471-479, 1995
 A>Title: Isolation and characterization of the chicken trypsinogen gene family.
 A:Reference number: S55066; MUID:95251611; PMID:7733885
 A:Accession: S55066
 A:Molecule type: mRNA

A;Title: The amino acid sequence of the gamma-subunit of mouse submaxillary gland 7 S N
A;Reference number: A92341; MUID:81264363; PMID:7263706
A;Accession: A92341
A:Molecule type: protein
A:Residues: 25-107,112-261 <THO>
A:Experimental source: outbred strain Swiss Webster
C;Comment: 7S nerve growth factor is composed of two alpha chains, a beta dimer composed
C;Comment: The active form of the gamma chain occurs naturally as combinations of either
C;Genetics:
A;Map position: 7
A;Introns: 16/1; 69/2; 165/1; 210/3
C;Superfamily: trypsin; trypsin homology
C;Keywords: glycoprotein; growth factor; hydrolase; serine proteinase; submandibular gla
F;1-18/Domain: signal sequence #status predicted <SIG>
F;25-253/Domain: trypsin homology <TRY>
F;45-107/Domain: segment B1 <GB1>
F;25-107,112-261/Product: nerve growth factor gamma chain (active form) #status experime
F;112-261/Domain: segment A <GAA>
F;112-164/Domain: segment C <GCC>
F;165-261/Domain: segment B2 <GB2>
F;31-173,50-66,152-219,184-198,209-234/Disulfide bonds: #status predicted
F;65,120,213/Active site: His, Asp, Ser #status predicted
F;102/Binding site: carboxylate (Asn) (covalent) #status experimental

Query Match 37.2%; Score 509; DB 1; Length 261;
Best Local Similarity 39.5%; Pred. No. 7,2e-37;
Matches 103; Conservative 48; Mismatches 86; Indels 24; Gaps 6;

QY 10 WFL-GVLIIGVAG-SLVSGSCQIINGEDCSPHSQPQAAQVMENELFCGVLVHPQWVL 67
Db 2 WLLIIFLALSLGIDAAPVQGRIVGGFKCKNNSQWVAVRYTYTLCGGVLLDPNWVL 61
QY 68 SAAHCFQNSYTTIGLHLSLEADQEPGSOVMVASLSVRHPPEYRPL-AND 116
Db 62 TAAHCYDDNVKYWLGNLTKD-EPASQHRFVSKAIPHPGFNMLMKHIRFLEYDYSND 120
QY 117 LMLIKLDESVSDDTIRTSISASQCTAGNSCLVSGWGLLANGRMPTVLQ-CVNV 170
Db 121 LMLRLSKPADITDTVKPITLTPBPGLGSTCLASGWSIT---PTKFQFTDLYCVNL 176
QY 171 SVYSBEVCSKLYDPLVHPSMFCAGGQDQKDCNGSDSGGFLICNGYLOGLVSPGKAPCGQ 230
Db 177 KULPNEDCAKAIHKVYTDMLCAGEMDGCKDKGSDSGFLICDGVLOGLVSGHTPCGE 236
QY 231 VGVPGVYTNLCKPTIEWIKTV 251
Db 237 PDMPGVYTNLCNKFTSWIKDTM 257

RESULT 7
A34079
tissue kallikrein (EC 3.4.21.35) P1 precursor - rat
N;Alternate names: kallikrein-related proteinase k8
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 22-Jun-1999
C;Accession: A34079; S10700
R;Brady, J.M.; Wines, D.R.; MacDonald, R.J.
Biochemistry 28, 5203-5210, 1989
A;Title: Expression of two kallikrein gene family members in the rat prostate.
A;Reference number: A34079; MUID:89352606; PMID:2765531
A;Accession: A34079
A;Status: preliminary
A:Molecule type: DNA: mRNA
A:Residues: 1-261 <BRA>
A;Cross-references: GB:M27215; GB:M27216; GB:M27217; NID:G206638; PIDN:AAA42036.1; PID:G206638
A;Experimental source: prostate
R;Elmoujahed, A.; Gutman, N.; Brillard, M.; Gauthier, P.
FEBS Lett. 265, 137-140, 1990
A;Title: Substrate specificity of two kallikrein family gene products isolated from the
A;Reference number: S10698; MUID:90306305; PMID:2194829
A;Accession: S10700
A:Molecule type: protein
A;Residues: 25-43;112-138 <ELM>

A, Experimental source: submaxillary gland

A, Note: 125-Lys was also found

C, Superfamily: trypsin; trypsin homology

C, Keywords: hydrolase; serine proteinase

F: 25-253/Domain: trypsin homology <TRY>

F: 25-111/Product: tissue kallikrein P1 light chain #status experimental <MAT1>

F: 112-261/Product: tissue kallikrein P1 heavy chain #status experimental <MAT2>

F: 165, 120, 213/Active site: His, Asp, Ser #status predicted

Query Match 37.0%; Score 507; DB 2; Length 261;

Best Local Similarity 42.2%; Pred. No. 1.1e-36;

Matches 100; Conservative 39; Mismatches 84; Indels 14; Gaps 3;

QY 29 SQIINGEDCSPHSQPQWQAALVMEELFCGVLVHPQWLSAAHCFQNSYITGLGLHSLA 88

DB 23 SRIIGGFNCKNSQWQVAVVHFNEPQCGGVLIHPSWVITAAHCYSYNYQWLGRLNLE 82

QY 89 DQEPSQMVSEASLSVRHPEYRNPIL-----ANDMLIKLDESSESDETIRISII 137

DB 83 D-EPPAQHRLVSQSPHFPFGFNLDIIKNHTRKPGNDYNDMLMLLTKTPADITDGVKVIDL 141

QY 138 ASQCTAGNSCLVSGWGLA--NGRMPTVLCQNVSVVSEBVCGLYDPLVHPSMFCAGG 195

DB 142 PTEEPKVSCTLTSGWGSITPLKFEFPDDLCQVNIHLLSNEKCIKAYNDEVTDVWLAGE 201

QY 196 GQDKDSCNGDSGGPLICNGVLVSGKAPCGQGVGVYTNLCKPTEWIEKTVQ 252

DB 202 MDGGKIDCKDGGGLICDGLVQITSGWSPCGEPNKPVSYYTKLIKFTSMKKVMK 258

RESULT 8

A27547

trypsin (EC 3.4.21.4) precursor, cationic - rat

C, Species: Rattus norvegicus (Norway rat)

C, Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 22-Jun-1999

C, Accession: A27547

R, Flecher, T.S.; Alhadeff, M.; Craik, C.S.; Laigman, C.

Biochemistry 26, 3081-3086, 1987

A, Title: Isolation and characterization of a cDNA encoding rat cationic trypsinogen.

A, Reference number: A27547; MUID: 87271609; PMID: 3607011

A, Accession: A27547

A, Molecule type: mRNA

A, Residues: 1-247 <FLE>

A, Cross-references: GB:M16624; NID:Q206498; PIDN:AAA41985.1; PID:G206499

C, Superfamily: trypsin; trypsin homology

C, Keywords: calcium binding; hydrolase; protein digestion; serine proteinase

F: 25-240/Domain: trypsin homology <TRY>

F: 31-161, 49-65, 133-234, 140-207, 172-186/Disulfide bonds: #status predicted

F: 64, 108, 201/Active site: His, Asp, Ser #status predicted

F: 76, 78, 81, 86/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Query Match 37.0%; Score 506; DB 2; Length 247;

Best Local Similarity 40.5%; Pred. No. 1.2e-36;

Matches 100; Conservative 50; Mismatches 89; Indels 8; Gaps 6;

QY 11 FLGYLLGVAGSL-VSGSCSQIINGEDCSPHSQPQWQAALVMEELFCGVLVHPQWLSA 69

DB 6 FLAF--LGRAVALPDDDDKIVGGYTCQKNSLPYQVSL-NAGYHFCGSLINSQWVSA 62

QY 70 AHCFQNSYITGLGLHSLAEDQEPGSQWVEASLSVRHPEYRNPILLANDMLIKLDESSES 129

DB 63 AHCKRSRIQVRLGEHNDV-VEGGEQFIDAAKIIRHPSYNANTFNDIMLIKNSPATIN 121

QY 130 DTIRSIASQCTAGNSCLVSGWGL--LLANGRMPTVLCQNVSVVSEBVCGLYDPLVH 187

DB 122 SRVSTVSLPRSCGSSGKCLVSGWGLTSLSGTNPSPILLQCLDAPVLSDSCKSSYPGKIT 181

QY 188 PSMFCAGGQDQKDCNCGDSGGPLICNGVLVSGKAPCGQGVGVYTNLCKPTEWIE 247

DB 182 SNMFCLFLGEGKDCSQDGGSGPWCNGQLQGVVSWGYG-CAQKGRPGVYTKVCNVVNI 240

QY 248 EKVQAS 254

:::|::|

DB 241 QQTVAAN 247

RESULT 9

S01971

tissue kallikrein (EC 3.4.21.35) precursor - mouse

N, Alternate names: glandular kallikrein

C, Species: Mus musculus (house mouse)

C, Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 21-Jul-2000

C, Accession: S01971; I70023

R, Drinkwater, C.C.; Richards, R.I.

Nucleic Acids Res. 16, 10318, 1988

A, Title: Sequence of mGK-11, a mouse glandular kallikrein gene.

A, Reference number: S01971; MUID: 89083511; PMID: 3205728

A, Accession: S01971

A, Molecule type: DNA

A, Residues: 1-261 <DRI>

A, Cross-references: EMBL:X13215; NID:G53064; PIDN:CAA31604.3; PID:G5708211

R, Evans, B.A.; Drinkwater, C.C.; Richards, R.I.

J. Biol. Chem. 262, 8027-8034, 1987

A, Title: Mouse glandular kallikrein genes: Structure and partial sequence analysis of th

A, Reference number: I55260; MUID: 87250386; PMID: 3036794

A, Accession: I70023

A, Status: preliminary; translated from GB/EMBL/DBJ

A, Molecule type: DNA

A, Residues: 70-122 <RES>

A, Cross-references: GB:M18610; NID:G198529; PIDN:AAA39353.1; PID:G198537

C, Genetics:

A, Introns: 16/1; 69/2; 165/1; 210/3

C, Superfamily: trypsin; trypsin homology

C, Keywords: hydrolase; serine proteinase

F: 1-17/Domain: signal sequence #status predicted <SIG>

F: 18-24/Domain: propeptide #status predicted <PRO>

F: 25-261/Product: tissue kallikrein #status predicted <MAT>

F: 25-253/Domain: trypsin homology <TRY>

F: 65, 120, 213/Active site: His, Asp, Ser #status predicted

Query Match 37.0%; Score 506; DB 2; Length 261;

Best Local Similarity 40.5%; Pred. No. 1.3e-36;

Matches 104; Conservative 43; Mismatches 94; Indels 16; Gaps 5;

QY 10 WFL-GYLLGVAG-SLVSGSCSQIINGEDCSPHSQPQWQAALVMEELFCGVLVHPQWVL 67

DB 2 WFLIFLALSGIDAAAPPVQSVGFNCKNSQWVHVAIVRYNKIICGVLLDRNWVL 61

QY 68 SAAHCFQNSYITGLGLHSLAEDQEPGSQWVEASLSVRHPEYRNPIL-----AND 116

DB 62 TAAACHVSOINVMWLGKTL-FOREPSAQHRMWSKSPHPDYNMSLLIHNPEDEDSND 120

QY 117 LMLIKLDESSESDETIRSIASQCTAGNSCLVSGWGLANGRM--PTVLQCVNVSWS 174

DB 121 LMLRLSEPADITDAVKPIALPTEEPKLGSTCLVSGWGSITPTKFTQDDLCQVSKLLP 180

QY 175 EEVCSKLYDPLVHPSMFCAGGQDQKDCNCGDSGGPLICNGVLVSGKAPCGQGVGP 234

DB 181 NEVCVKHNOKVTDVMLCAGEMGGGKDTCKGDSGGPLICDGVLHGITAWGPIPGKENTP 240

QY 235 GVTNLCCKFTWIEKTV 251

DB 241 GVTKLKFTNWKDTM 257

RESULT 10

JE0236

tissue kallikrein (EC 3.4.21.35) - mouse

N, Alternate names: prorenin-converting enzyme

C, Species: Mus musculus (house mouse)

C, Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jul-2000

C, Accession: JE0236

R, Hosoi, K.; Tada, J.; Teamura, K.; Kanamori, N.; Yamanaka, N.

J. Biochem. 124, 368-376, 1998

A, Title: Expression of an allzyme of prorenin-converting enzyme in the submandibular gl

A, Reference number: JE0236; MUID: 98351995; PMID: 9685728

QY 133 RSISASOCTAGNSCLVSGWGLLNG-RMPTVLQCVNVSVSEVCKLYDPLVHPMSF 191
Db 125 STIPLPQVCTAGTECLVSGWGLVLFKFPESPSVLCQLDAPVLSVSVCHKAYPRQITNNMF 184
QY 192 CAGGQDQKSCNDGSGGGLICNGYLQGLVSGFSGKAPCGQGVGPVYNNLCKFTWIEKTV 251
Db 185 CLGFLGGKDSQYDVGSGPVVGVNGEVQVSGWGDG-CALEGKPGVYTKVCNLYNLNWIQTV 243
QY 252 QAS 254
Db 244 AAN 246

RESULT 13

A29586
tissue kallikrein (EC 3.4.21.35) hGK-1 precursor - human

N/Alternate names: glandular kallikrein

C/Species: Homo sapiens (man)

C/Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 22-Jun-1999

C/Accession: A29586

R/Schedlich, L.J.; Bennetts, B.H.; Morris, B.J.

DNA 6, 429-437, 1987

A/Title: Primary structure of a human glandular kallikrein gene.

A/Reference number: A29586; MUID:88054467; PMID:2824146

A/Accession: A29586

A/Molecule type: DNA

A/Residues: 1-261 <SCH>

A/Cross-references: GB:M18157; NID:G186640; PIDN:AAA4454.1; PID:G386842

A/Note: the authors translated the codon TAC for residue 43 as Trp

C/Genetics:

A/Introns: 16/1; 69/2; 165/1; 210/3

C/Superfamily: trypsin; trypsin homology

C/Keywords: hydrolase; serine proteinase

F:25-253/Domain: trypsin homology <TRY>

F:65,120,213/Active site: His, Asp, Ser #status predicted

Query Match 36.7%; Score 502.5; DB 2; Length 261;

Best Local Similarity 38.7%; Pred. No. 2.7e-36;

Matches 101; Conservative 44; Mismatches 91; Indels 25; Gaps 5;

QY 15 LILVAGSLVSGSC-----SQTINGEDCSPHSQPQWQAALVWENELFCGVLVHPQWV 66

Db 4 LVLSTA---LSVGCYGAFLIQSRIVGGWCEKHSQPMQVAVYSGHWAHCGGLVHPQWV 60

QY 67 LSAAHCFQNSYITIGLHLSLEADQEPGQSMVEASLSVRHPEYRPLL-----AN 115

Db 61 LTAACHLKNSQVWLGRNLFEPEDTG-QRVFVSHSFPHLYNNLLKHQSLRDEDSH 119

QY 116 DLMLIKLDESVSSEDTIRISIASOCTAGNSCLVSGWGLLANGRM--PTVLQCVNVSV 173

Db 120 DLMLRLSEPAKITDVVKVLGPTQEPALGTTCTYASGWGSTPEBFLRPRSLQCVSLHL 179

QY 174 SEVCSKLYDPLVHPMSFCAGGQDQKSCNGDSGGPLICNGYLQGLVSGFKAPCGQGV 233

Db 180 SNDMCARAYSEKVTFFMLCAGLWTCGDKTCGGDSGLPLVNCVLQGLITSWGPFCALPEK 239

QY 234 PGVYTNLCKFTWIEKTVQAS 254

Db 240 PAVYTKVHYRQWIKDTAAN 260

QY 234 PGVYTNLCKFTWIEKTVQAS 254

Db 240 PAVYTKVHYRQWIKDTAAN 260

QY 234 PGVYTNLCKFTWIEKTVQAS 254

Db 240 PAVYTKVHYRQWIKDTAAN 260

RESULT 14

A41020

tissue kallikrein (EC 3.4.21.35) mGK-13 precursor - mouse

N/Alternate names: epidermal growth factor-binding protein type B; prorenin-converting

C/Species: Mus musculus (house mouse)

C/Date: 13-May-1992 #sequence_revision 13-May-1992 #text_change 22-Jun-1999

C/Accession: A41020; B29746; PC2014; I70027; SI8674

R/Kim, W.S.; Nakayama, K.; Nakagawa, T.; Kawamura, Y.; Haraguchi, K.; Murakami, K.

J. Biol. Chem. 266, 19283-19287, 1991

A/Title: Mouse submandibular gland prorenin-converting enzyme is a member of glandular

A/Reference number: A41020; MUID:92011720; PMID:1918045

A/Accession: A41020

A/Molecule type: mRNA
A/Residues: 1-261 <KIM>
A/Cross-references: GB:X56628; NID:G53771; PIDN:CAA41482.1; PID:G53772
R/Drinkwater, C.C.; Evans, B.A.; Richards, R.I.

Biochemistry 26, 6750-6756, 1987

A/Title: Mouse glandular kallikrein genes: identification and characterization of the ge

A/Reference number: A90522; MUID:88107594; PMID:3322387

A/Accession: B29746

A/Molecule type: DNA

A/Residues: 1-118, 'D', 120-261 <DRI>

A/Experimental source: strain BALB/c, salivary gland

R/Hosoi, K.; Tsunashima, S.; Kurihara, K.; Aoyama, H.; Ueha, T.; Sakiyama, F.

J. Biochem. 115, 137-143, 1994

A/Title: Identification of mk1, a true tissue (glandular) kallikrein of mouse submandib

A/Reference number: PC2013; MUID:94245648; PMID:8188620

A/Accession: PC2014

A/Molecule type: Protein

A/Residues: 25-58, 'X', 60-66; 165-206 <HOS>

A/Experimental source: submandibular gland

R/Drinkwater, C.C.; Richards, R.I.

J. Biol. Chem. 262, 8027-8034, 1987

A/Title: Mouse glandular kallikrein genes: structure and partial sequence analysis of th

A/Reference number: I55260; MUID:87250386; PMID:3036794

A/Accession: I70027

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 70-122 <RES>

A/Cross-references: GB:M18612; NID:G198533; PIDN:AAA39354.1; PID:G198538

C/Genetics:

A/Gene: mk13

C/Superfamily: trypsin; trypsin homology

C/Keywords: hydrolase; saliva; serine proteinase; submandibular gland

F:25-253/Domain: trypsin homology <TRY>

F:65,120,213/Active site: His, Asp, Ser #status predicted

Query Match 36.7%; Score 502; DB 2; Length 261;

Best Local Similarity 40.1%; Pred. No. 2.9e-36;

Matches 103; Conservative 44; Mismatches 94; Indels 16; Gaps 5;

QY 10 WEL-GYLLIGVAG-SLVSGSCSQIINGEDCSPHSQPQWQAALVWENELFCGVLVHPQWV 67

Db 2 WFLILFALSLGIDNAPPLQSRVVGFGFNCKNSQPMQVAVYQKEHICGVLLENWVL 61

QY 68 SAAHCFQNSYITIGLHLSLEADQEPGQSMVEASLSVRHPEYRPLL-----AND 116

Db 62 TAAHCYVDQYEWLGNKVL-FQEPQAQHLVSKSPFHPGFNNLLMLQTIIPGADFND 120

QY 117 LMLIKLDESVSSEDTIRISIASOCTAGNSCLVSGWGLLANGR--MPTVLQCVNVSV 174

Db 121 LMLRLSEPAKITDVVKVLGPTQEPALGTTCTYASGWGSTPEBFLRPRSLQCVSLHL 180

QY 175 EEVCSKLYDPLVHPMSFCAGGQDQKSCNGDSGGPLICNGYLQGLVSGFKAPCGQGV 234

Db 181 NENCAKVIQKVTDMVLCAGWGGKDTCTDDSGGPLICDGLQGTTSYGPVPCGKPGVP 240

QY 235 GVTNLCFTWIEKTV 251

Db 241 AIYTNLIKFNWIKDTM 257

QY 235 GVTNLCFTWIEKTV 251

Db 241 AIYTNLIKFNWIKDTM 257

QY 235 GVTNLCFTWIEKTV 251

Db 241 AIYTNLIKFNWIKDTM 257

RESULT 15

T01779

trypsin (EC 3.4.21.4) - plaice

C/Species: Pleuronectes platessa (plaice)

C/Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 16-Jul-1999

C/Accession: T01779

R/Leaver, M.J.; George, S.G.

submitted to the EMBL Data Library, March 1996

A/Reference number: Z14422

A/Accession: T01779

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A:Residues: 1-250 <LEA>
A:Cross-references: EMBL:X56744; NID:g1213630; PID:g64240
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; protein digestion; serine proteinase
F:23-242/Domain: trypsin homology <TRY>

Query Match 36.6%; Score 501.5; DB 2; Length 250;
Best Local Similarity 42.3%; Pred. No. 3.1e-36;
Matches 105; Conservative 37; Mismatches 97; Indels 9; Gaps 5;

QY	12	LGVLILGVAGSLVSGSCQIINGEDCSPHSQPWQAALVMENELFCSGVLVHPQWVLSAAH	71
Db	4	LALLMVGAAVAVPREDGRIIGGHECAHSRPFMASLNYGH-FCGGVLINNQWVLSVAH	62
QY	72	CFONSYT--IGLGLHLEADQEPGQWVEASLSVRHPEYNRPILLANDLMLIKLDESVSSES	129
Db	63	CWYNPAMQVNLGEHDLR-KFEGTEQLMKTDITIIHPNIDYQTLDFDINLILKLYHPEVVS	121
QY	130	DTIRISIASQCPTAGNSCLVSGWGLLANG----RMPTVLQCVNVSWSVEEVCCKLYDPL	185
Db	122	HAVGPIPLPTSCPVAGTPCSVSGWGNRTARDGEVYLPTLLQCMDFIVDDEQCMKSYDDM	181
QY	186	YHPSMEFCAGGGQDKSCNGDSGGLICNGYLGQVLSFGKAPCGQGVGVGVVTLNCKPTE	245
Db	182	ISPRMYCAGFMDGSRDCAACNGDSGLVCRGEVYGLVSWGQG-CAQPNYPGVVYVYKLCBFLG	240
QY	246	WIEKTVQA	253
Db	241	WIERLEA	248

Search completed: May 5, 2004, 16:09:56
Job time : 21 secs


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FT CHAIN 31 254 ENAMEL MATRIX SERINE PROTEINASE 1.
SQ SEQUENCE 254 AA; 27235 MW; FD40EF85664406F1 CRC64;

Query Match 81.3%; Score 1113; DB 6; Length 254;
Best Local Similarity 77.68; Pred. No. 4.2e-99;
Matches 197; Conservative 26; Mismatches 31; Indels 0; Gaps 0;

QY 1 MATAGNPGWPLGVLILGVAGSLVSGSCQIINGEDCSPHSQWQAALVWENELFCGVL 60
DB 1 MTAAGNPGWPLGVLILGVAGSLVSGSCQIINGEDCSPHSQWQAALVWENELFCGVL 60
QY 61 VHPQWVLSAAHCFQNSYTIIGLHSLADQPGSQWVEASLSVRHPEYNRLPLANDMLI 120
DB 61 VHPQWVLSAAHCFQNSYTIIGLHSLADQPGSQWVEASLSVRHPEYNRLPLANDMLI 120
QY 121 KLDESVSSEDTIRISIASQCTAGNSCLVSGWGLLANGRMPTVLCQNVSVSEVCSK 180
DB 121 KLDESVSSEDTIRISIASQCTAGNSCLVSGWGLLANGRMPTVLCQNVSVSEVCSK 180
QY 121 KLKESVLSLDTYRNISVSVQCFTPGDSCLVSGMGLASGLRLPQLVLCQWISVASEEYCKA 180
DB 121 KLKESVLSLDTYRNISVSVQCFTPGDSCLVSGMGLASGLRLPQLVLCQWISVASEEYCKA 180
QY 181 LYDPLXHPSPMFCAGGGQDKDSCNGSDGGPLICNGYLQGLVSGFKAPCGGVGVYTNL 240
DB 181 RYGVVYHPSPMFCAGGGQDKDSCNGSDGGPLICNGYLQGLVSGFKAPCGGVGVYTNL 240
QY 241 CKFTWIEKTVQAS 254
DB 241 CKFTDWIQTITQAS 254

RESULT 2
Q96JEO PRELIMINARY; PRT; 205 AA.
AC Q96JEO;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE ARML.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=prostate tumor xenograft;
RX MEDLINE=21398046; PubMed=11506707;
RA Korkmaz K.S., Korkmaz C.G., Pretlow T.G., Saatcioglu F.;
RT "Distinctly different gene structure of KLK4/KLK-Li/Protease/ARML compared with other members of the kallikrein family - Perinuclear localization, alternative cDNA forms and regulation by multiple hormones.";
RT localizaation, alternative cDNA forms and regulation by multiple hormones.";
RL DNA Cell Biol. 20:435-445(2001).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AF259966; AAK71702.1; -.
DR HSSP; P00761; 1ANL.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS0240; TRYPsin_DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; 1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
KW Hydrolyase; Protease; Serine protease.
SQ SEQUENCE 205 AA; 21950 MW; B83A025C73DBA1F6 CRC64;

Query Match 80.2%; Score 1098; DB 4; Length 205;
Best Local Similarity 100.0%; Pred. No. 9.1e-98;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FT CHAIN 31 254 ENAMEL MATRIX SERINE PROTEINASE 1.
SQ SEQUENCE 254 AA; 27235 MW; FD40EF85664406F1 CRC64;

Query Match 81.3%; Score 1113; DB 6; Length 254;
Best Local Similarity 77.68; Pred. No. 4.2e-99;
Matches 197; Conservative 26; Mismatches 31; Indels 0; Gaps 0;

QY 1 MATAGNPGWPLGVLILGVAGSLVSGSCQIINGEDCSPHSQWQAALVWENELFCGVL 60
DB 1 MTAAGNPGWPLGVLILGVAGSLVSGSCQIINGEDCSPHSQWQAALVWENELFCGVL 60
QY 61 VHPQWVLSAAHCFQNSYTIIGLHSLADQPGSQWVEASLSVRHPEYNRLPLANDMLI 120
DB 61 VHPQWVLSAAHCFQNSYTIIGLHSLADQPGSQWVEASLSVRHPEYNRLPLANDMLI 120
QY 121 KLDESVSSEDTIRISIASQCTAGNSCLVSGWGLLANGRMPTVLCQNVSVSEVCSK 180
DB 121 KLDESVSSEDTIRISIASQCTAGNSCLVSGWGLLANGRMPTVLCQNVSVSEVCSK 180
QY 121 KLKESVLSLDTYRNISVSVQCFTPGDSCLVSGMGLASGLRLPQLVLCQWISVASEEYCKA 180
DB 121 KLKESVLSLDTYRNISVSVQCFTPGDSCLVSGMGLASGLRLPQLVLCQWISVASEEYCKA 180
QY 181 LYDPLXHPSPMFCAGGGQDKDSCNGSDGGPLICNGYLQGLVSGFKAPCGGVGVYTNL 240
DB 181 RYGVVYHPSPMFCAGGGQDKDSCNGSDGGPLICNGYLQGLVSGFKAPCGGVGVYTNL 240
QY 241 CKFTWIEKTVQAS 254
DB 241 CKFTDWIQTITQAS 254

RESULT 2
Q96JEO PRELIMINARY; PRT; 205 AA.
AC Q96JEO;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE ARML.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=prostate tumor xenograft;
RX MEDLINE=21398046; PubMed=11506707;
RA Korkmaz K.S., Korkmaz C.G., Pretlow T.G., Saatcioglu F.;
RT "Distinctly different gene structure of KLK4/KLK-Li/Protease/ARML compared with other members of the kallikrein family - Perinuclear localization, alternative cDNA forms and regulation by multiple hormones.";
RT localizaation, alternative cDNA forms and regulation by multiple hormones.";
RL DNA Cell Biol. 20:435-445(2001).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AF259966; AAK71702.1; -.
DR HSSP; P00761; 1ANL.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS0240; TRYPsin_DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; 1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
KW Hydrolyase; Protease; Serine protease.
SQ SEQUENCE 205 AA; 21950 MW; B83A025C73DBA1F6 CRC64;

Query Match 80.2%; Score 1098; DB 4; Length 205;
Best Local Similarity 100.0%; Pred. No. 9.1e-98;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 MENELFCGVLVHPQWVLSAAHCFQNSYTIIGLHSLADQPGSQWVEASLSVRHPEYN 109
DB 1 MENELFCGVLVHPQWVLSAAHCFQNSYTIIGLHSLADQPGSQWVEASLSVRHPEYN 60
QY 110 RPLANDMLIKLDESVSSEDTIRISIASQCTAGNSCLVSGWGLLANGRMPTVLCQVN 169
DB 61 RPLANDMLIKLDESVSSEDTIRISIASQCTAGNSCLVSGWGLLANGRMPTVLCQVN 120
QY 170 VSVVSEVCSKLYDPLXHPSPMFCAGGGQDKDSCNGSDGGPLICNGYLQGLVSGFKAPCG 229
DB 121 VSVVSEVCSKLYDPLXHPSPMFCAGGGQDKDSCNGSDGGPLICNGYLQGLVSGFKAPCG 180
QY 230 QVGPVGVTNLCKFTWIEKTVQAS 254
DB 181 QVGPVGVTNLCKFTWIEKTVQAS 205

RESULT 3
Q96JEO PRELIMINARY; PRT; 205 AA.
AC Q96JEO;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE ARML.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=prostate;
RX MEDLINE=21398046; PubMed=11506707;
RA Korkmaz K.S., Korkmaz C.G., Pretlow T.G., Saatcioglu F.;
RT "Distinctly different gene structure of KLK4/KLK-Li/Protease/ARML compared with other members of the kallikrein family - Perinuclear localization, alternative cDNA forms and regulation by multiple hormones.";
RT localizaation, alternative cDNA forms and regulation by multiple hormones.";
RL DNA Cell Biol. 20:435-445(2001).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AF259964; AAK71700.1; -.
DR HSSP; P00761; 1ANL.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS0240; TRYPsin_DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; 1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
KW Hydrolyase; Protease; Serine protease.
SQ SEQUENCE 205 AA; 22052 MW; 159B61A20D94BD57 CRC64;

Query Match 79.4%; Score 1087; DB 4; Length 205;
Best Local Similarity 99.0%; Pred. No. 1e-96;
Matches 203; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 50 MENELFCGVLVHPQWVLSAAHCFQNSYTIIGLHSLADQPGSQWVEASLSVRHPEYN 109
DB 1 MENELFCGVLVHPQWVLSAAHCFQNSYTIIGLHSLADQPGSQWVEASLSVRHPEYN 60
QY 110 RPLANDMLIKLDESVSSEDTIRISIASQCTAGNSCLVSGWGLLANGRMPTVLCQVN 169
DB 61 RPLANDMLIKLDESVSSEDTIRISIASQCTAGNSCLVSGWGLLANGRMPTVLCQVN 120
QY 170 VSVVSEVCSKLYDPLXHPSPMFCAGGGQDKDSCNGSDGGPLICNGYLQGLVSGFKAPCG 229
DB 121 VSVVSEVCSKLYDPLXHPSPMFCAGGGQDKDSCNGSDGGPLICNGYLQGLVSGFKAPCG 180

```


01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enamel matrix serine proteinase 1 precursor.
GN KLK4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP "Localization of Emsp1 expression during tooth formation and cloning of mouse cDNA."
RL J. Dent. Res. 79:70-76(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss-Webster;
RX MEDLINE=20152522; PubMed=10690663;
RA Hu J.C., Ryu O.H., Chen J.J., Uchida T., Wakida K., Murakami C., Jiang H., Qian Q., Zhang C., Otmiers V., Bartlett J.D., Simmer J.P.;
RT "Localization of Emsp1 expression during tooth formation and cloning of mouse cDNA."
RT in developing mouse incisors."
RL Gene 251:1-8(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss-Webster;
RX MEDLINE=20323211; PubMed=10863090;
RA Hu J.C., Zhang C., Sun X., Yang Y., Cao X., Ryu O., Simmer J.P.;
RT "Characterization of the mouse and human PRSS17 genes, their relationship to other serine proteases, and the expression of PRSS17 in developing mouse incisors."
RL Gene 251:1-8(2000).
RN [2]
RP SEQUENCE FROM N.A.
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AF019979; AAC98894.1; -.
DR HSSP; P00763; 1DPO.
DR MEROPS; S01.251; -.
DR MGD; MGI:1861379; KLK4.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin_1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hyaluronase; Protease; Serine protease; Signal.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 32 255 MATRIX SERINE PROTEINASE 1.
SQ SEQUENCE 255 AA; 27488 MW; 6FD2E7DEA0660A2A CRC64;
Query Match 72.7%; Score 995; DB 11; Length 255;
Best Local Similarity 69.3%; Pred. No. 1e-87;
Matches 176; Conservative 31; Mismatches 47; Indels 0; Gaps 0;
QY 1 MATAGNPGWFLGVLILVAGSLVSGSCQIINGEDCSPHSQPQWQAALVMENELFCSGVL 60
DB 2 MVTARTPGWFLGLILEVTGASASSVSSRIQGDSCPSHQPQWQAALFSGEDFCGVL 61
QY 61 VHPQWLVAACFQNSYITIGLHSLVAGSLVSGSCQIINGEDCSPHSQPQWQAALVMENELFCSGVL 120
DB 62 VHPQWLVAACFQNSYITIGLHSLVAGSLVSGSCQIINGEDCSPHSQPQWQAALFSGEDFCGVL 121
QY 121 KLDESVSDDTIRSIASQCTAGNSCLVSGWGLANGRMPTVLCQNVSVVSEECVSK 180
DB 122 KLVESVIESNIRSFVATQCTPGTCLVSGWGLKNGKLPVSLQCVNLVSAEETCRL 181
QY 181 LYDPLVHPMFAGGQDQKDCNCGDGGPLICNGYQGLVSGFKAPCGQGVGVGYVTNL 240
DB 182 LYDPVTHLMFACGAGGQDQKDCNCGDGGPVCNRSQGLVSMGQKCGQGPVGYVTNL 241
QY 241 CKFTWIKTVQAS 254
DB 242 CKFTNWIQTIGTN 255

RESULT 7
Q96PTO PRELIMINARY; PRT; 195 AA.
AC Q96PTO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Kallikrein 4 splice variant.
GN KLK4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99367447; PubMed=10438493;
RA Stephenson S.A., Verity K., Ashworth L.K., Clements J.A.;
RT "Localization of a new prostate-specific antigen-related serine protease gene, KLK4, is evidence for an expanded human kallikrein gene family cluster on chromosome 19q13.3-13.4."
RL J. Biol. Chem. 274:23210-23214(1999).
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AF148532; AAL14782.1; -.
DR HSSP; P00761; 1AN1.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin_1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hyaluronase; Protease; Serine protease.
SQ SEQUENCE 195 AA; 20585 MW; EF7E96978B1515B1 CRC64;
Query Match 61.9%; Score 848; DB 4; Length 195;
Best Local Similarity 97.6%; Pred. No. 1.1e-73;
Matches 160; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 MATAGNPGWFLGVLILVAGSLVSGSCQIINGEDCSPHSQPQWQAALVMENELFCSGVL 60
DB 1 MATAGNPGWFLGVLILVAGSLVSGSCQIINGEDCSPHSQPQWQAALVMENELFCSGVL 60
QY 61 VHPQWLVAACFQNSYITIGLHSLVAGSLVSGSCQIINGEDCSPHSQPQWQAALVMENELFCSGVL 120
DB 62 VHPQWLVAACFQNSYITIGLHSLVAGSLVSGSCQIINGEDCSPHSQPQWQAALVMENELFCSGVL 120
QY 121 KLDESVSDDTIRSIASQCTAGNSCLVSGWGLANGRMPTV 164
DB 121 KLDESVSDDTIRSIASQCTAGNSCLVSGWGLANGELTGV 164
RESULT 8
Q96PTI PRELIMINARY; PRT; 159 AA.
AC Q96PTI;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Kallikrein 4 splice variant.
GN KLK4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99367447; PubMed=10438493;
RA Stephenson S.A., Verity K., Ashworth L.K., Clements J.A.;

RT "Localization of a new prostate-specific antigen-related serine protease gene, KLK4, is evidence for an expanded human kallikrein gene family cluster on chromosome 19q13.3-13.4.";

RT J. Biol. Chem. 274:23210-23214 (1999).

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

DR EMBL; AF148532; AA114781.1; -

DR HSP; P00761; 1AN1.

DR GO; GO:0004263; F:chymotrypsin activity; IEA.

DR GO; GO:0008233; F:peptidase activity; IEA.

DR GO; GO:0004295; F:trypsin activity; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro; IPR009003; Cys Ser trypsin.

DR InterPro; IPR001254; Peptidase_S1.

DR Pfam; PF00089; trypsin_1.

DR PRINTS; PR00722; CHYMOTRYPSIN.

DR SMART; SM00020; TRYPSIN_DOM; 1.

DR PROSITE; PS00240; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_HIS; 1.

KW Hydrolase; Protease; Serine protease.

SQ SEQUENCE 159 AA; 16931 MW; 3CC66BF49136CA5A CRC64;

Query Match 61.7%; Score 845; DB 4; Length 159;

Best Local Similarity 100.0%; Pred. No. 1.7e-73;

Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATAGNPGWFLGYLLGVAGSLVSGSCQIINGDCSPHSQPWQAALVWENELFCGVL 60

DB 1 MATAGNPGWFLGYLLGVAGSLVSGSCQIINGDCSPHSQPWQAALVWENELFCGVL 60

QY 61 VHPQWVLSAAHCFQNSVTIGLHLSLEADQEPGQSMVEASLSVHPHPEYNPLANDMLI 120

DB 61 VHPQWVLSAAHCFQNSVTIGLHLSLEADQEPGQSMVEASLSVHPHPEYNPLANDMLI 120

QY 121 KLDSVESDPTIRISIASOCPAGNSCLVSGWGLLANG 159

DB 121 KLDSVESDPTIRISIASOCPAGNSCLVSGWGLLANG 159

RESULT 9

Q96JDB PRELIMINARY; PRT; 131 AA.

AC Q96JDB

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE ARM1 (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CK NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Prostate;

RC MEDLINE=21398046; PubMed=11506707;

RA Korkmaz K.S., Korkmaz C.G., Perlow T.G., Saatcioglu F.;

RT "Distinctly different gene structure of KLK4/CLK-11/Protease/ARM1 compared with other members of the kallikrein family - Perinuclear localization, alternative cDNA forms and regulation by multiple hormones.";

RT DNA Cell Biol. 20:435-445 (2001).

RL -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

CC EMBL; AF259968; AAK71704.1; -

DR HSP; P00761; 1AN1.

DR GO; GO:0004263; F:chymotrypsin activity; IEA.

DR GO; GO:0008233; F:peptidase activity; IEA.

DR GO; GO:0004295; F:trypsin activity; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro; IPR009003; Cys Ser trypsin.

DR InterPro; IPR001254; Peptidase_S1.

DR Pfam; PF00089; trypsin_1.

DR PRINTS; PR00722; CHYMOTRYPSIN.

DR SMART; SM00020; TRYPSIN_DOM; 1.

DR PROSITE; PS00240; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_HIS; 1.

KW Hydrolase; Protease; Serine protease.

FT NON TER 131 131

SQ SEQUENCE 131 AA; 14107 MW; 03434B6D95AF2406 CRC64;

Query Match 49.3%; Score 675; DB 4; Length 131;

Best Local Similarity 100.0%; Pred. No. 3.3e-57;

Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 MENELFCGVLVHPQWVLSAAHCFQNSVTIGLHLSLEADQEPGQSMVEASLSVHPHPEYN 109

DB 1 MENELFCGVLVHPQWVLSAAHCFQNSVTIGLHLSLEADQEPGQSMVEASLSVHPHPEYN 60

QY 110 RPLLANDMLIKLDSVESDPTIRISIASOCPAGNSCLVSGWGLLANGRMTVLQCVN 169

DB 61 RPLLANDMLIKLDSVESDPTIRISIASOCPAGNSCLVSGWGLLANGRMTVLQCVN 120

QY 170 VSVVSEEVCS 179

DB 121 VSVVSEEVCS 130

RESULT 10

Q9DI40 PRELIMINARY; PRT; 293 AA.

AC Q9DI40

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE 1110030019RIK protein.

DE 1110030019RIK.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

CK NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Embryo;

RC MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,

RA Saico T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Stauber F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Marzarelli J., Monbets P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690 (2001).

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

DR EMBL; AK003996; BAB23113.1; -

DR HSP; P00763; 1DPO.

DR MEROPS; S01.017; -

DR MEROPS; S01.418; -

DR MGD; MGI:131518; 1110030019RIK.

DR GO; GO:0004263; F:chymotrypsin activity; IEA.

DR GO; GO:0008233; F:peptidase activity; IEA.

DR GO; GO:0004295; F:trypsin activity; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro; IPR009003; Cys Ser trypsin.

DR InterPro; IPR001254; Peptidase_S1.

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DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSIN_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Hydroxylase; Protease; Serine protease.
SQ SEQUENCE 293 AA; 31908 MW; EDIF45D8226FE911 CRC64;

Query Match 46.6%; Score 637.5; DB 11; Length 293;
Best Local Similarity 41.5%; Pred No. 3.7e-53;
Matches 122; Conservative 51; Mismatches 80; Indels 41; Gaps 5;

QY 1 NATAGNPGWFLGYLI-----LGVAGSLVSG----- 26
DB 1 MARIHPKWKAMATLITLVLGSPVLADGVSSCDNPSGTPSGTNRDLSTDSKSGEDT 60
QY 27 ---SCSQTINGEDCSPHSQPQQAALVM-ENELFCGVLVHPQWLVAHCFQNSYITIGL 82
DB 61 RSDSSRIIVSGDCKQKQAPQWGLLGNKLYCGAVLSPQWLTAHCKKPVFRILG 120
QY 83 LHSLEADQEPGQMVVEASLSVRHPEYNRPLLANDMLIKLDESVSSESDTIRSIASQCP 142
DB 121 HHSMSPVVEGQMPQGIKSIPIHPGYSHPGSHNDMLIKMKRKIRDSHVKPVEIADCA 180
QY 143 TAGNSCLVSGWGLL--ANGRMPTVLQVNVSVVSEVCSKLYDPLVHPSMFCAGGGQDQK 200
DB 181 TEGTRCMVSGWGTTSSTSHNNPKVLQCLNITVLSSECKNSYPQCIDKTMFCA-GDBEGR 239
QY 201 DSCNGSDGGLTCNGYLGVLVSFGKAPCGQVGVVYTNLCKFTWIEKTVQAS 254
DB 240 DSCQDGGPVPVCGKGLGVSWGDFPCCAQNRNRPQVYTNLCEFEVKWIKDTMNSN 293

RESULT 11
Q96JD7 PRELIMINARY; PRT; 146 AA.
AC Q96JD7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ARM1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=prostate tumor xenograft;
RX Korkmaz K.S.; Korkmaz C.G.; Pretlow T.G.; Saatcioglu F.;
RT "Distinctly different gene structure of KLK4/KLK-L1/Protease/ARM1
RT compared with other members of the kallikrein family - Perinuclear
RT localization, alternative cDNA forms and regulation by multiple
RT hormones.";
RL DNA Cell Biol. 20:435-445(2001).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AF259970; AAK71705.1; -.
DR HSP; P00761; 1AN1.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0004295; F:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSIN_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR Hydroxylase; Protease; Serine protease.
KW

SQ SEQUENCE 269 AA; 29226 MW; D3C1E1FBEEA3634C CRC64;

Query Match 42.0%; Score 575; DB 4; Length 269;
Best Local Similarity 43.9%; Pred. No. 3.5e-47;
Matches 118; Conservative 42; Mismatches 69; Indels 40; Gaps 6;

QY 1 MATAGNPGWFLGYLI-----LGV-----AGSLVSG----- 26
DB 1 MATARPPWVWVLCALITALLGVTEHVLANNVSDHPSNTVPSGNSQDLGAGAGEDARS 60
QY 27 ---SCSQTINGEDCSPHSQPQQAALVM-NEELFCGVLVHPQWLVAHCFQNSYITIGL 83
DB 61 DSSSRRIIVSGDCKQKQAPQWGLLGNKLYCGAVLSPQWLTAHCKKPVFRILG 120
QY 84 HSLLEADQEPGQMVVEASLSVRHPEYNRPLLANDMLIKLDESVSSESDTIRSIASQCP 143
DB 121 YLSLPVVEGQMPQGIKSIPIHPGYSHPGSHNDMLIKMKRKIRDSHVKPVEIADCA 180
QY 144 AGNSCLVSGWGLLGRM--PTVLQCVNVSVVSEVCSKLYDPLVHPSMFCAGGGQDQK 201

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Db 181 AGTKCLVSGGTTKSPQVHPFKVLQCLNLSVLQKRCEDAYPRQIDDTWFCAGDRAKGRD 239
Qy 202 SCNGDSGGLICNGYLQGLVSGFKAPCGQ 230
Db 240 SCQDSGSGPVVCGSLQGLVSGWDYFCAR 268

RESULT 13
Q96RUS PRELIMINARY; PRT; 110 AA.
AC Q96RUS;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2003 (TREMBlrel. 25, Last annotation update)
DE ARMI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=21398046; PubMed=11506707;
RA Korkmaz K.S., Korkmaz C.G., Prelow T.G., Saatcioglu F.;
RT "Distinctly different gene structure of KLK4/CLK-L1/protease/ARMI
RT compared with other members of the kallikrein family - Perinuclear
RT localization, alternative cDNA forms and regulation by multiple
RT hormones.";
RL DNA Cell Biol. 20:435-445(2001).
CC -|- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AF259971; AAK71706.1; -.
DR HSP; P00761; IAN1.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004395; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPsin.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 110 AA; 11858 MW; B6F9C135EA93B116 CRC64;

Query Match 41.9%; Score 574; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.5e-47;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 50 MENELFCGVLVHPQWVLSAAHCFQNSYITGLGHSLEADQEPGQWVEASLSVRHPEYN 109
Db 1 MENELFCGVLVHPQWVLSAAHCFQNSYITGLGHSLEADQEPGQWVEASLSVRHPEYN 60

Qy 110 RPLANDMLIKLDESVSSEDTTIRSISIASQCTAGNSCLVSGWGLANG 159
Db 61 RPLANDMLIKLDESVSSEDTTIRSISIASQCTAGNSCLVSGWGLANG 110

RESULT 14
Q8EN9 PRELIMINARY; PRT; 253 AA.
AC Q8EN9;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Kallikrein 7 (chymotryptic, stratum corneum).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
```

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RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
CC -|- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; BC032005; AAH32005.1; -.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPsin.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 253 AA; 27608 MW; 2D68B6A41B22A668 CRC64;

Query Match 40.7%; Score 556.5; DB 4; Length 253;
Best Local Similarity 45.8%; Pred. No. 2e-45;
Matches 110; Conservative 40; Mismatches 83; Indels 7; Gaps 4;

Qy 15 LILGAGSLVSGSCQIINGEDCSPHSQPQWQALVMENELFCSGLVHPQWVLSAAHCFQ 74
Db 16 LALETAGEAQG--DKIIDGAPCARGHPQWQVALLSGNQLHCGGVLVNERWLTAAHCKM 73

Qy 75 NSYITGLGHSLEADQEPGQWVEASLSVRHPEYNRPLANDMLIKLDESVSSEDTIRS 134
Db 74 NEYTVHLGSDTL-GDRL--AQIRAKSRFRPGYSTQTHVNDLMLVKLSQARLSMYVK 130

Qy 135 ISIASQCTAGNSCLVSGWGLANG--RMPTVLCVNVSVVSEVCSKLYDPLVHPSMFC 192
Db 131 VRLPSRCEPPTGTTCTVSGWGTTPDPTFSPDLACVDVKLISPDQCTKYKDLLENMLC 190

Qy 193 AGGGQDQKDCNGSDGGGLICNGYLQGLVSGFKAPCGQWVGVVYTNLCKTEMIETVQ 252
Db 191 AGIPDSKKNACNGSDGGGLVCRGTIQLGVLVSGTFFWGPDPGVTYQVCKTKINDMK 250

RESULT 15
Q7TIR8 PRELIMINARY; PRT; 242 AA.
AC Q7TIR8;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Trypsinogen.
OS Pangasius hypophthalmus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Pangasidae; Pangasius.
OX NCBI_TaxID=85560;
RN [1]
SEQUENCE FROM N.A.
RA Moreau Y., Avarre J.-C., Cahu C., Suryanti Y., Utami R.;
RT "Characterization of trypsin and cDNA encoding trypsinogen in a
RT pangasidae, Pangasius hypophthalmus.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY316360; AAP81159.1; -.
SQ SEQUENCE 242 AA; 26361 MW; 17D9B1F71B085B06 CRC64;

Query Match 39.5%; Score 540.5; DB 13; Length 242;
Best Local Similarity 42.4%; Pred. No. 6.6e-44;
Matches 101; Conservative 54; Mismatches 74; Indels 9; Gaps 5;

Qy 23 LVSSC-----SQIINGEDCSPHSQPQWQALVMENELFCSGLVHPQWVLSAAHCFQNSY 77
Db 8 LLVGACFALEDKDKVGGVECTPSQWQVSLNVGYH-FCGSLINQNMWWSAAHCFQNSRI 66
```

Qy 78 TIGLHLSLEADQEPGQWVSEASVVRHPEYNREPLANDLMLIKLDESSESITRSISI 137
Db 67 EVRLGEHNIQIN-EGTEQFISRRVIRHPNYSWTIDIMLIKLSQASVNNYVOPVAL 125
Qy 138 ASQCFTAGNSCLVSGWG-LLANGEMPTVLQCVNYSVVSEVCSKLYDPLYPMSMFCAGGG 196
Db 126 PSSCFFPAGTWCIVSGWNTMSTADRNKLQCEVFPILSDEDCNNSYFCNITKAMFCAGFL 185
Qy 197 QDQKDSGNGDSGGLICNGYLQGLVSPFKAPCGQGVGVVYTNLCFTWIEKTVQAS 254
Db 186 EGGKDSGQDGGPWCNGELQGVSWGYG-CAEKNHFGVYTKVCIETDWAQTIASN 242

Search completed: May 5, 2004, 16:09:24
Job time : 47 secs

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OM protein - protein search, using sw model

Run on: May 5, 2004, 15:55:17 ; Search time 17 Seconds
(without alignments)
777.989 Million cell updates/sec

Title: US-09-895-814-525

Perfect score: 1369

Sequence: 1 MATAGNPGWFLGLVILGVA.....GVYNLCKFTWIEKTVQAS 254

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1369	100.0	254	1 KLK4 HUMAN	Q9Y5K2 homo sapien
2	671	49.0	293	1 NRPN RAT	Q9Y337 homo sapien
3	569.5	41.6	260	1 KLN5 HUMAN	O88780 rattus norv
4	567.5	41.5	253	1 KLN7 HUMAN	P49862 homo sapien
5	563.5	41.2	260	1 NRPN MOUSE	P61955 mus musculus
6	549	40.1	250	1 KLN8 HUMAN	Q9UBX7 homo sapien
7	535.5	39.1	251	1 KLN6 HUMAN	Q9P0G3 homo sapien
8	517.5	37.8	277	1 KLN9 HUMAN	Q9UKR3 homo sapien
9	515.5	37.7	260	1 KLN8 HUMAN	O60259 homo sapien
10	515	37.6	244	1 KLN4 RAT	P36375 rattus norv
11	510.5	37.3	248	1 TRV3 CHICK	Q90629 gallus gall
12	509	37.2	261	1 KLN3 MOUSE	P00756 mus musculus
13	507	37.0	261	1 KLN8 RAT	P36374 rattus norv
14	506.5	37.0	244	1 KLN6 HUMAN	Q92876 homo sapien
15	506	37.0	247	1 TRV3 RAT	P08426 mus musculus
16	506	37.0	261	1 KLN8 MOUSE	P15946 mus musculus
17	503	36.7	261	1 KLN7 RAT	P36373 rattus norv
18	502.5	36.7	246	1 TRV2 HUMAN	P32822 rattus norv
19	502.5	36.7	261	1 KLN2 HUMAN	P20151 homo sapien
20	502	36.6	261	1 KLN3 MOUSE	P36368 mus musculus
21	499.5	36.5	246	1 TRV1 CANFA	P06871 canis fami
22	498	36.4	248	1 KLN6 HUMAN	Q9UKR0 homo sapien
23	498	36.4	256	1 KLN6 HUMAN	Q9H2R5 homo sapien
24	498	36.4	261	1 KLN3 HUMAN	P07288 homo sapien
25	497	36.3	247	1 TRV4 RAT	P12788 rattus norv
26	496	36.3	259	1 KLN3 RAT	P36376 rattus norv
27	496	36.2	248	1 TRV2 CHICK	Q90628 gallus gall
28	496	36.2	259	1 KLN6 MOUSE	P15948 mus musculus
29	496	36.2	261	1 KLN1 RAT	P00758 rattus norv
30	495.5	36.2	246	1 TRV1 RAT	P32821 rattus norv
31	493.5	36.0	248	1 TRV1 CHICK	Q90627 gallus gall
32	493	36.0	244	1 TRV2 XENLA	P70059 xenopus lae
33	492.5	36.0	261	1 KLN9 MOUSE	P15949 mus musculus

ALIGNMENTS

RESULT 1

ID	KLK4 HUMAN	STANDARD;	PRT;	254 AA.
AC	Q9Y5K2; Q9GZL6; Q9UBJ6;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Kallikrein 4 precursor (EC 3.4.21.-) (protease) (Kallikrein-like protein 1) (KLK-Li) (Enamel matrix serine proteinase 1).			
GN	KLK4 OR PRS17 OR PSTS OR ENSPI.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
LN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99179024; PubMed=10077646;			
RA	Nelson P.S., Gan L., Ferguson C., Moss P., Gelinas R., Hood L.,			
RA	Wang K.,			
RT	"Molecular cloning and characterization of prostate, an androgen-regulated serine protease with prostate-restricted expression.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 96:3114-3119(1999).			
LN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99413477; PubMed=10485467;			
RA	Yousef G.M., Obezu C.V., Luo L.-Y., Black M.H., Diamandis E.P.;			
RT	"Protease/KLK-Li is a new member of the human kallikrein gene family, is expressed in prostate and breast tissues, and is hormonally regulated.";			
RL	Cancer Res. 59:4252-4256(1999).			
LN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99367447; PubMed=10438493;			
RA	Stephenson S.A., Verity K., Ashworth L.K., Clements J.A.;			
RT	"Localization of a new prostate-specific antigen-related serine protease gene, KLK4, is evidence for an expanded human kallikrein gene family cluster on chromosome 19q13.3-13.4.";			
RL	J. Biol. Chem. 274:23210-23214(1999).			
LN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20510030; PubMed=11054574;			
RA	Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,			
RA	Moss P., Paepser B., Wang K.;			
RT	"Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region.";			
RL	Gene 257:119-130(2000).			
LN	[5]			
RP	SEQUENCE FROM N.A.			
RA	Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,			
RA	Burkhardt-Schultz K.J., Gordon L., Dias J., Ramirez M., Stillwagen S.,			
RA	Phan H., Velasco N., Do L., Regala W., Terry A., Ganes J., Liu S.,			
RA	Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,			
RA	Attix C., Andreise T., Trankheim M., Amico-Keller G., Coefield J.,			
RA	Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,			
RA	Arellano A., Brower A., Sanders C., Ow D., Nolan M., Trong S.,			
RA	Kobayashi A., Olsen A.S., Carrano A.V.;			

Q07276 macaca fasc
P36369 mus musculus
P15947 mus musculus
P00760 bos taurus
Q28773 papio hamad
P06870 homo sapien
P00762 rattus norv
P33619 macaca mlla
P00759 rattus norv
P15945 mus musculus
Q29463 bos taurus
P00755 mus musculus

34 492 35.9 257 1 KLN1 MACPA
35 491 35.9 261 1 KLN2 MOUSE
36 489.5 35.8 261 1 KLN6 MOUSE
37 488.5 35.7 243 1 TRV1 BOVIN
38 488.5 35.7 258 1 KLN1 PAPHAN
39 487.5 35.6 262 1 KLN1 HUMAN
40 485 35.4 246 1 TRV1 RAT
41 485 35.4 261 1 KLN3 MACMU
42 484 35.4 259 1 KLN2 RAT
43 484 35.4 261 1 KLN5 MOUSE
44 480 35.1 247 1 TRV2 BOVIN
45 480 35.1 261 1 KLN1 MOUSE

"Sequence analysis of a 4.8 MB region of 19q13.4 between KLK1 and SYT3.";
 Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 [6]
 RN SEQUENCE OF 22-254 FROM N.A.
 RA Simmer J.P., Ryu O.H., Qian Q., Zhang C., Cao X., Sun X., Hu C.-C.;
 RT "Cloning and characterization of a cDNA encoding human EMSPI.";
 RL (In) Goldberg M. (eds.);
 RL Chemistry and biology of mineralized tissues, pp.1-1, American
 RL Academy of Orthopaedic Surgeons, Vittel (2000).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed in prostate.
 CC -!- SIMILARITY: Belongs to peptidase family S1. kallikrein subfamily.
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 CC
 CC EMBL; AF113140; RAD21580.1; -;
 CC EMBL; AF113141; AAD21581.1; -;
 CC EMBL; AF135023; AAD26424.2; -;
 CC EMBL; AF148532; AAD38019.1; -;
 CC EMBL; AF243527; AAG33357.1; -;
 CC EMBL; AC037199; -; NOT ANNOTATED_CDS.
 CC EMBL; AF126401; AAG43246.1; -;
 CC HSSP; P00763; LDPO.
 CC MEROPS; S01.251; -;
 CC Genew; HGNC:6365; KLK4.
 CC MIM; 603767; -;
 CC GO; GO:0005615; C:extracellular space; TAS.
 CC GO; GO:0008236; F:serine-type peptidase activity; TAS.
 CC InterPro; IPR009003; Cys Set trypsin.
 CC InterPro; IPR001254; Peptidase S1.
 CC InterPro; IPR001314; Peptidase_S1A.
 CC Pfam; PF00089; trypsin; 1.
 CC PRINTS; PR00722; CHYMOTRYPSIN.
 CC SMART; SM00020; Tryp_SPC; 1.
 CC PROSITE; PS02040; TRYPSIN_DOM; 1.
 CC PROSITE; PS00134; TRYPSIN_HIS; 1.
 CC PROSITE; PS00135; TRYPSIN_SER; 1.
 CC Hydrolase; Serine protease; Zymogen; Signal.
 KW SIGNAL 1 26
 FT PROPEP 27 30 POTENTIAL.
 FT CHAIN 31 254 KALLIKREIN 4.
 FT ACT_SITE 71 71 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 116 116 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 207 207 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 37 167 BY SIMILARITY.
 FT DISULFID 56 72 BY SIMILARITY.
 FT DISULFID 141 241 BY SIMILARITY.
 FT DISULFID 148 213 BY SIMILARITY.
 FT DISULFID 178 192 BY SIMILARITY.
 FT DISULFID 203 228 BY SIMILARITY.
 FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 197 197 Q -> H (IN REF. 1 AND 4).
 SQ SEQUENCE 254 AA; 27022 MW; 9C475E22B6EE0CB8 CR664;
 Query Match 100.0%; Score 1369; DB 1; Length 254;
 Best Local Similarity 100.0%; Pred. No. 4.8e-116;
 Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MATAGNFWGFLGLVAGSLVSGSCQIINGEDCSHSPQWQALVWNEPFCSGVL 60
 DB 1 MATAGNFWGFLGLVAGSLVSGSCQIINGEDCSHSPQWQALVWNEPFCSGVL 60
 QY 61 VHPQWVLSAHCQNSYITIGLHSLSEADQEPGQVMEASLSVRHPEYNRPFLANDLMI 120
 DB 61 VHPQWVLSAHCQNSYITIGLHSLSEADQEPGQVMEASLSVRHPEYNRPFLANDLMI 120

QY 121 KLDESVSSESDTIRISISIASQCPTAGNSCLVSGWGLLANGMPVTLQCVNVSVSEVCSK 180
 DB 121 KLDESVSSESDTIRISISIASQCPTAGNSCLVSGWGLLANGMPVTLQCVNVSVSEVCSK 180
 QY 181 LYDPLVHPNMFAGGGQDQKSDGNSGSPGLICNGYLQGLVSGFKAPCGQGVPGVYTNL 240
 DB 181 LYDPLVHPNMFAGGGQDQKSDGNSGSPGLICNGYLQGLVSGFKAPCGQGVPGVYTNL 240
 QY 241 CKFTEWIEKTVQAS 254
 DB 241 CKFTEWIEKTVQAS 254
 RESULT 2
 KLK5 HUMAN STANDARD; PRT; 293 AA.
 ID Q9V37; Q9HBG8;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Kallikrein 5 precursor (EC 3.4.21.-) (Stratum corneum tryptic enzyme)
 DE (Kallikrein-like protein 2) (KLK-L2).
 GN KLK5 OR SCTE.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Stratum Corneum;
 RX MEDLINE=99445563; PubMed=10514489;
 RA Brattsand M., Egelrud T.;
 RT "Purification, molecular cloning, and expression of a human stratum
 RT corneum trypsin-like serine protease with possible function in
 RT desquamation.";
 RL J. Biol. Chem. 274:30033-30040(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20118156; PubMed=10652563;
 RX Yousef G.M., Luo L.-Y., Diamandis E.P.;
 RA "Identification of novel human kallikrein-like genes on chromosome
 RA 19q13.3-q13.4.";
 RL Anticancer Res. 19:2843-2852(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20510030; PubMed=11054574;
 RX Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
 RA Moss P., Paepel B., Wang K.;
 RT "Sequencing and expression analysis of the serine protease gene
 RT cluster located in chromosome 19q13 region.";
 RL Gene 257:119-130(2000).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=2238257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein J.J., Udwin T.B., Toshivuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length

```

Db      181  AGTKCLVSGWGTTSQVHFPPKVQLCINLSVLSQKRCEDAYPRQIDDTMCA-GDKAGRD 233
Qy      202  SCNGDSGGPLICNGYLGVLVFGKAPCGQGVPGVYTNLCKFTIEWIKTVOAS 254
        |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      240  SCQDSGGPVVCGNSLQGLVSGWGDYPCARPNRPVYTNLCKFTKWIQETIQAN 292

RESULT 3
NRPN RAT      STANDARD;      PRT;      260 AA.
AC      O88780;
AD      15-JUL-1999 (Rel. 38, Created)
DT      15-JUL-1999 (Rel. 38, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Neuropilin precursor (EC 3.4.21.-) (NP) (Kallikrein 8) (Brain serine
DE      protease 1).
DE      GN KX8 OR PRSS19 OR NRPN OR BSP1.
OS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
SEQUENCE FROM N.A.
RC      STRAIN=Fischer; TISSUE=Brain;
RX      MEDLINE=98389725; PubMed=9722524;
RA      Davies B.J., Pickard B.S., Steel M., Morris R.G.M., Lathe R.;
RT      "Serine proteases in rodent hippocampus.";
RT      J. Biol. Chem. 273:23004-23011(1998).
CC      -1- FUNCTION: Suggested to be involved in kindling epileptogenesis and
CC      hippocampal plasticity. Has a strong proteolytic activity against
CC      fibronectin (By similarity).
CC      -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
CC      -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC      -1- TISSUE SPECIFICITY: Restricted to hippocampus.
CC      -1- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.
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CC      -----
CC      EMBL; AJ005641; CAA06643.1; -
CC      HSP; Q61955; INPM.
CC      MEROPS; S01.244; -.
DR      InterPro; IPR009003; Cys Ser trypsin.
DR      InterPro; IPR001254; Peptidase_S1.
DR      InterPro; IPR001314; Peptidase_S1A.
DR      Pfam; PF00089; trypsin; 1.
DR      PRINTS; PR00722; CHYMOTRYPSIN.
DR      SMART; SM00020; Tryp_SPC; 1.
DR      PROSITE; PS00240; TRYPSIN_DOM; 1.
DR      PROSITE; PS00134; TRYPSIN_HIS; 1.
DR      PROSITE; PS00135; TRYPSIN_SER; 1.
KW      Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal.
FT      SIGNAL          1 28      POTENTIAL.
FT      PROPEP         29 32      BY SIMILARITY.
FT      CHAIN          33 260     NEUROPSIN.
FT      ACT_SITE       73 73      CHARGE RELAY SYSTEM (BY SIMILARITY).
FT      ACT_SITE      120 120     CHARGE RELAY SYSTEM (BY SIMILARITY).
FT      ACT_SITE      212 212     CHARGE RELAY SYSTEM (BY SIMILARITY).
FT      DISULFID       39 173     BY SIMILARITY.
FT      DISULFID       58 74      BY SIMILARITY.
FT      DISULFID      145 246     BY SIMILARITY.
FT      DISULFID      152 218     BY SIMILARITY.
FT      DISULFID      184 198     BY SIMILARITY.
FT      DISULFID      208 233     BY SIMILARITY.
FT      CARBOHYD       110 110     N-LINKED (GLCNAC...) (POTENTIAL).
SQ      SEQUENCE      260 AA; 56DF4F602A0B7F5 CRC64;
Query Match          41.6%; Score 569.5; DB 1; Length 260;

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Db 131 VRLPSRCEPPTCTVSGWGTTSPTDVTFFSDLMCDVDKLI SPQDCTKVKYKDLLENSMLC 190
 Qy 193 AGGGQDKDNGSDGGLPLCNGLVQLVSGFKAPCGQGVGVYNNLCKFTWISKTQV 252
 Ds 191 AGIPDSKKNACNGSDGGLPLCRGLTGLVSGWTFPCQPNPDPGVYTVQCKFTKWIINDTWK 250

RESULT 5
 NRPN MOUSE
 ID NRPN MOUSE STANDARD; PRT; 260 AA.
 AC Q61955;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Neuprosin precursor (EC 3.4.21.-) (NP) (Kallikrein 8).
 GN KIK8 OR PRS19 OR NRPN
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C; TISSUE=Hippocampus;
 RX MEDLINE=95348817; PubMed=7623137;
 RA Chen Z.-L., Yoshida S., Kato K., Momota Y., Suzuki J., Tanaka T.,
 RA Ito J., Nishino H., Amoto S., Kiyama H., Shiosaka S.;
 RT "Expression and activity-dependent changes of a novel limbic-serine
 RT protease gene in the hippocampus.";
 RL J. Neurosci. 15:5088-5097(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yoshida S., Hirata A., Inoue N., Shiosaka S.;
 RT "Cloning and assignment of mouse neuropein gene, Prs19 to chromosome
 RT 7B4.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Czech II; TISSUE=Mammary gland;
 RX MEDLINE=23388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Hopkins R.F., Jordan H., Korte T., Farmer A.A., Rubin G.M., Hong L.,
 RA Datchenko L., Marusina K., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fanev J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP SEQUENCE OF N-TERMINUS, AND CHARACTERIZATION.
 RC STRAIN=BALB/C; TISSUE=Brain;
 RX MEDLINE=98225202; PubMed=9556608;
 RA Shimizu C., Yoshida S., Shibata M., Kato K., Momota Y., Matsumoto K.,
 RA Shiosaka T., Midorikawa R., Kamachi T., Kawabe A., Shiosaka S.;
 RT "Characterization of recombinant and brain neuropein, a
 RT plasticity-related serine protease.";
 RL J. Biol. Chem. 273:11189-11196(1998).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 33-257.
 RC TISSUE=Hippocampus;
 RX MEDLINE=99134351; PubMed=9933620;
 RA Kishi T., Kato M., Shimizu T., Kato K., Matsumoto K., Yoshida S.,

Shiosaka S., Hakoshima T.;
 RT "Crystal structure of neuropein, a hippocampal protease involved in
 RT kindling epileptogenesis.";
 RL J. Biol. Chem. 274:4220-4224(1999).
 CC -!- FUNCTION: Suggested to be involved in kindling epileptogenesis and
 CC hippocampal plasticity. Has a strong proteolytic activity against
 CC fibronectin.
 CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
 CC -!- ENZYME REGULATION: Strongly inhibited by diisopropyl
 CC fluorophosphate, leupeptin and (4-aminophenyl)methanesulfonyl 1-
 CC fluoride.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed specifically in the limbic system of
 CC mouse brain and is localized at highest concentration in pyramidal
 CC neurons of the hippocampal CA1-3 subfields.
 CC -!- MASS SPECTROMETRY: MW=26613; METHOD=MALDI; RANGE=29-260.
 CC -!- MASS SPECTROMETRY: MW=26229; METHOD=MALDI; RANGE=33-260.
 CC -!- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.
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 CC -----
 CC EMBL; D30785; BAA06451.1; -;
 CC EMBL; AB032202; BAA92435.1; -;
 CC EMBL; BC055895; AAH55895.1; -;
 CC PIR; I56559; I56559.
 CC PDB; INFM; 23-MAR-99.
 CC MEROPS; S01.244; -;
 CC MGD; MGI:892018; Kik8.
 CC InterPro; IPR009003; Cys Ser trypsin.
 CC InterPro; IPR01254; Peptidase S1.
 CC InterPro; IPR001314; Peptidase_S1A.
 CC Pfam; PF00089; trypsin; 1.
 CC PRINTS; PR00722; CHYMOTRYPSIN.
 CC SMART; SM00020; Tryp_SPC; 1.
 CC PROSITE; PS00240; TRYPSIN_DOM; 1.
 CC PROSITE; PS00134; TRYPSIN_HIS; 1.
 CC PROSITE; PS00135; TRYPSIN_SER; 1.
 CC Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal;
 KW 3D-structure. 1 28
 FT SIGNAL 1 28
 FT PROPEP 29 32
 FT CHAIN 33 260
 FT ACT_SITE 73 73
 FT ACT_SITE 120 120
 FT ACT_SITE 212 212
 FT DISULFID 39 173
 FT DISULFID 58 74
 FT DISULFID 145 246
 FT DISULFID 152 218
 FT DISULFID 184 198
 FT DISULFID 208 233
 FT CARBOHYD 110 110
 FT STRAND 34 34
 FT STRAND 37 38
 FT TURN 41 42
 FT TURN 45 46
 FT STRAND 47 52
 FT TURN 53 54
 FT STRAND 55 64
 FT TURN 65 66
 FT STRAND 72 74
 FT STRAND 80 83
 FT STRAND 87 87
 FT TURN 88 89
 FT STRAND 96 98
 FT STRAND 100 105
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CHARGE RELAY SYSTEM (BY SIMILARITY).

FT TURN 107 108
 FT TURN 114 115
 FT TURN 118 119
 FT STRAND 122 126
 FT STRAND 140 141
 FT STRAND 148 149
 FT STRAND 151 156
 FT STRAND 170 170
 FT STRAND 172 178
 FT HELIX 181 187
 FT TURN 189 191
 FT TURN 194 195
 FT STRAND 196 200
 FT TURN 202 203
 FT STRAND 206 206
 FT TURN 209 210
 FT TURN 212 213
 FT STRAND 215 218
 FT TURN 219 220
 FT STRAND 221 228
 FT STRAND 235 235
 FT TURN 236 237
 FT STRAND 238 238
 FT STRAND 240 244
 FT HELIX 245 256
 SQ SEQUENCE 260 AA; 28523 MW; B5F6F6BE37CD60B CRC64;

Query Match 41.2%; Score 563.5; DB 1; Length 260;
 Best Local Similarity 41.3%; Pred. No. 1.7e-43;
 Matches 102; Conservative 47; Mismatches 91; Indels 7; Gaps 4;

QY 10 WFLGVLILVAGSVSGSCQIINGEDCSPHSQPQWQAALVMEFLFSGVLVHPQWVLSA 69
 DB 12 WILLLFPWAGLITRAQGSKILSGRECIPHSQPQWQAALFQGERLICGGVLVGRWVLT 71
 QY 70 AHCFQNSVTIGLHLSLEADOPGQSVVEASLVRFHYRPL---LANDMLIKLDES 126
 DB 72 AHCKKQKYSVLGSHLSQSRDQP-EQIQAQSIQHPCYNNSPEDSHDMLIRLQNSA 130
 QY 127 SESDTIRISIASOCPTAGNSCLVSGWGLLANGR--NPTVLQCVNVSWSEEVCSKLYDP 184
 DB 131 NLGDKVKEVQANLCPKVGQKCIISGWTVTSPENFNTLCAEVLKYSQNKCEAYPG 190
 QY 185 LYHPSMFCAGGQDQKSCNDSGGGLICNGLVLSFGKAPCGQVGVGVYTNLCCKFT 244
 DB 191 KITGEWCA-GSSNGADTCQSDSGPLVCDMLQGITWSGSDPCGKPKFVYTKICRYT 249
 QY 245 EWIEKTV 251
 DB 250 TWIKTKM 256

RESULT 6
 ID KLCB HUMAN STANDARD; PRT; 250 AA.
 AC Q9UBX7, O75837; Q9NS65;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Kallikrein 11 precursor (EC 3.4.21.-) (Hippostasin) (Trypsin-like protease)
 GN KLK11 OR PRSS20 OR TLSP.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Hippocampus;
 RX MEDLINE=98439738; PubMed=9765601;
 RA Yoshida S., Taniguchi M., Suemoto T., Oka T., He X.P., Shiozaka S.;
 RT "cDNA cloning and expression of a novel serine protease, TLSP.",
 RL Biochim. Biophys. Acta 1399:225-228(1998).

RA [2] SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Hippocampus, and Prostate;
 RX MEDLINE=20329229; PubMed=10872828;
 RA Mitsui S., Yamada T., Okui A., Komihama K., Uemura H., Yamaguchi N.;
 RT "A novel isoform of a kallikrein-like protease, TLSP/hippostasin, (PRSS20), is expressed in the human brain and prostate.";
 RL Biochem. Biophys. Res. Commun. 272:205-211(2000).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=20130117; PubMed=10662548;
 RA Yousef G.M., Scorialas A., Diamandis E.P.;
 RT "Genomic organization, mapping, tissue expression, and hormonal regulation of trypsin-like serine protease (TLSP PRSS20), a new member of the human kallikrein gene family.";
 RL Genomics 63:88-96(2000).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=20510030; PubMed=11054574;
 RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J., Moss P., Baepar B., Wang K.;
 RT "Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region.";
 RL Gene 257:119-130(2000).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong T.E., Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Prange C., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Mullahy S.J., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Gunaratne P.H., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gay L.J., Hulyk S.W., Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
 CC -1- FUNCTION: Possible multifunctional protease. Efficiently cleaves bz-Phe-Arg-4-methylcoumaryl-7-amide, a kallikrein substrate, and weakly cleaves other substrates for kallikrein and trypsin.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q9UBX7-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9UBX7-2; Sequence=VSP 005402;
 CC -1- TISSUE SPECIFICITY: Expressed in brain, skin and prostate. Isoform 1 is expressed preferentially in brain; isoform 2 in prostate.
 CC -1- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.

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CC -----
CC EMBL; AB012917; BAA33404.1; ALT_INIT.
CC EMBL; AB013730; BAA88713.1; -
CC EMBL; AB041036; BAA96797.1; -
CC EMBL; AF164623; AAD47815.1; -
CC EMBL; AF243527; AAG33364.1; -
CC EMBL; AC011473; AAG23257.1; -
CC EMBL; BC022068; AAH22068.1; -
CC HSP; P00763; IDPO.
CC MERO9; S01.257; -
CC Genew; HGNC:6359; KLK11.
CC MIM; 604434; -
CC GO; GO:0008236; F:serine-type peptidase activity; TAS.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SMC0020; Tryp_Src; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Glycoprotein; Signal; Zymogen;
KW Alternative splicing
FT SIGNAL 1 18 POTENTIAL.
FT PROPEP 19 21 ACTIVATION PEPTIDE (POTENTIAL).
FT CHAIN 22 250 KALLIKREIN 11.
FT ACT_SITE 62 62 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 110 110 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 203 203 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 28 163 BY SIMILARITY.
FT DISULFID 47 63 BY SIMILARITY.
FT DISULFID 135 237 BY SIMILARITY.
FT DISULFID 142 209 BY SIMILARITY.
FT DISULFID 174 188 BY SIMILARITY.
FT DISULFID 199 224 BY SIMILARITY.
FT CARBOHYD 99 99 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPITC 1 1 M -> MORLRWRDMSKSGRLTAKEPGARSPLOAM
FT FTid=VSP_005402.
SQ SEQUENCE 250 AA; 27466 MW; 192D910BDCD7A56 CRC64;
Query Match 40.1%; Score 549; DB 1; Length 250;
Best Local Similarity 41.7%; Pred. No. 3.3e-42;
Matches 103; Conservative 52; Mismatches 84; Indels 8; Gaps 4;
QY 12 LGYLILGAGSLVSGSCQIINGDCSPHSOPQAAALVMEELPCSGVLVHPQWVLSAAH 71
DB 4 LQILLALATGLVGE-TRIKGECKPSPQWQAALFEKTRLLCGATLAPRWLLTAH 62
QY 72 CFQNSYITGLGHLSEADQEPGSQNVASUSVRPEVNRPI-----LANDMLKLDESUS 127
DB 63 CLKPRYIVHLQHNLQ-KEEGCEQTRTATESFPHPGFNNSLPNKRDNDMLVMAASPVS 121
QY 128 ESDTIRTSIASOCPATGNSCLVSGWGLANG--RMPVTLCQNVSVVSEVCSKLYDPL 185
DB 122 ITWAVRPULSRVCVTAGTSLISGWGSTSPQRLPHTLRCAITIIIEHQKCNAYPGN 181
QY 186 YHPSMFCAGGGQDQKDSQNGSGGGLICNGYLGSLVGFQKAPCCQGVGVYVNLCKFTE 245
DB 182 ITDTWVCASVQEGGKDSQCGSGGGLVNCVNSQSLQGIISGWQDPCAITRKPGYTKVCKYVD 241

QY 246 WIEKTQV 252
DB 242 WIEQTMK 248
RESULT 7
KLKE_HUMAN
ID KLKE_HUMAN STANDARD; PRT; 251 AA.
AC Q9POG3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Kallikrein 14 precursor (EC 3.4.21.-) (Kallikrein-like protein 6)
DE (KLK-L6).
GN KLK14 OR KLK16.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Yousef G.M., Diamandis E.P.;
RT "Molecular characterization, mapping, and tissue expression of KLK16,
RT a hormonally regulated kallikrein-like gene.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. AND TISSUE SPECIFICITY.
RX MEDLINE=2125097; PubMed=11352573;
RA Hooper J.D., Bui L.T., Rae F.K., Harvey T.J., Myers S.A.,
RA Ashworth L.K., Clements J.A.;
RT "Identification and characterization of KLK14, a novel kallikrein
RT serine protease gene located on human chromosome 19q13.4 and expressed
RT in prostate and skeletal muscle.";
RL Genomics 73:117-122(2001).
RN [3]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Ganes J.,
RA Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
RA Andreise T., Frankheim M., Attix C., Amico-Keller G., Cosfield J.,
RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
RA Olsen A.S., Carrano A.V.;
RT "Sequence analysis of chromosome 19q13.4.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP TISSUE SPECIFICITY.
RX MEDLINE=20545474; PubMed=10969073;
RA Harvey T.J., Hooper J.D., Myers S.A., Stephenson S.A., Ashworth L.K.,
RA Clements J.A.;
RT "Tissue-specific expression patterns and fine mapping of the human
RT kallikrein (KLK) locus on proximal 19q13.4.";
RL J. Biol. Chem. 275:37397-37406(2000).
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- TISSUE SPECIFICITY: High expression in brain, bone marrow and
CC fetal liver. Also expressed in liver, pancreas, fetal spleen,
CC prostate and skeletal muscle.
CC -!- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.
CC -----
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CC -----
CC EMBL; AF161221; AAD50773.2; -
CC EMBL; AF283669; AAK48523.1; -
CC EMBL; AF283670; AAK48524.1; -
CC EMBL; AC011473; AAG23260.1; -
CC HSP; P00763; IDPO.

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DR MEROPS; S01.029; -
DR Genew; HGNC:6362; KLK14.
DR MIM; 606135; -
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0004252; F:serine-type endopeptidase activity; NAS.
DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR KW Hydrolyase; Serine protease; Signal; Zymogen.
FT SIGNAL 1 18
FT CHAIN 19 24
FT ACT_SITE 25 251
FT ACT_SITE 67 67
FT ACT_SITE 111 111
FT ACT_SITE 204 204
FT DISULFID 31 164
FT DISULFID 52 68
FT DISULFID 143 210
FT DISULFID 175 189
FT DISULFID 200 225
SQ SEQUENCE 251 AA; 27452 MW; 9087953BAFAVED25 CRC64;

Query Match 39.1%; Score 535.5; DB 1; Length 251;
Best Local Similarity 43.9%; Pred. No. 5.5e-41;
Matches 107; Conservative 34; Mismatches 92; Indels 11; Gaps 4;

Qy 16 ILGVAGSLVSGSCQIINGEDCSFHSQWQAALVM--ENLFCGVLVHPQWLVAHCF 73
Db 10 VLAIAMTQSDENKIKGGTCTTSQFQWQAALLAGPRRFLCGALLSGQWVITAAHCG 69

Qy 74 QNSVTIGLHSL--EADQPGQWYEASLSVRHPEYNRPLLANDLMLKLDSEVSSED 130
Db 70 RPILQVALGXENLRWEATQ---QVLVRVQVTHPEYNSTRHDNDLMLLQQLQPARIGR 125

Qy 131 TIRISIASOCTAGNCLVSGWGLLAN--GRMTPTVLQCNVSVSEVCSKLYDPLVHP 188
Db 126 AVRPIETVQACSPGTSRCVSGWTISPIARYPASLQCVNINISPDVEVCQKAYPRITTP 185

Qy 189 SMFAGGQDQDKSCNGDSGGPLCNGVLQGLVSGFKAPCGQVGVGVNLCFKFTWIE 248
Db 186 GMVAGVPGGKDSQGGSGPLVCRGQLQGLVSGWGMERCALPGYGVYVNLCKYRSWIE 245

Qy 249 KTVQ 252
Db 246 ETMR 249

RESULT 8
ID KLKD HUMAN STANDARD; PRT; 277 AA.
AC Q9UKR3; Q9Y433;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Kallikrein 13 precursor (EC 3.4.21.-) (Kallikrein-like protein 4)
DE (KLK-L4).
GN KLK13 OR KLK14.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20229789; PubMed=10766816;
RX Yousef G.M., Chang A., Dianandis E.P.;
RT "Identification and characterization of KLK-L4, a new kallikrein-like
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RT gene that appears to be down-regulated in breast cancer tissues.";
RL J. Biol. Chem. 275:11891-11898(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Carnes J.,
RA Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
RA Andreise T., Frankheim M., Attix C., Amico-Keller G., Cosfield J.,
RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
RA Olsen A.S., Garrano A.V.;
RA "Sequence analysis of chromosome 19q13.4.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 1-180 FROM N.A.
RC TISSUE=Uterus;
RA Ansonge W., Wirkner U., Mewes H.-W., Gassenhuber J., Wiemann S.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -|- SUBCELLULAR LOCATION: Secreted (Probable).
CC -|- TISSUE SPECIFICITY: Expressed in prostate, breast, testis and
CC salivary gland.
CC -|- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.
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CC
DR EMBL; AF135024; AAD26425.2; -
DR EMBL; AC011473; AAG23259.1; -
DR EMBL; AL050220; CAB43320.1; ALT_INIT.
DR HSP; P00763; IDPO.
DR MEROPS; S01.306; -
DR Genew; HGNC:6361; KLK13.
DR MIM; 605505; -
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0004252; F:serine-type endopeptidase activity; NAS.
DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR KW Hydrolyase; Serine protease; Glycoprotein; Signal.
FT SIGNAL 1 16
FT CHAIN 17 277
FT ACT_SITE 76 76
FT ACT_SITE 124 124
FT ACT_SITE 218 218
FT DISULFID 42 178
FT DISULFID 61 77
FT DISULFID 157 224
FT DISULFID 189 203
FT DISULFID 214 239
FT CARBOHYD 30 30
FT CARBOHYD 225 225
FT CONFLICT 170 180
SQ SEQUENCE 277 AA; 30570 MW; BABA9B8DCFB5D542 CRC64;

Query Match 37.8%; Score 517.5; DB 1; Length 277;
Best Local Similarity 41.1%; Pred. No. 2.6e-39;
Matches 108; Conservative 46; Mismatches 90; Indels 19; Gaps 7;

Qy 7 PWGFWFLGVLGVAGSLVSGSCQIN-----GDCSPHSQWQAALVMENLEFC 56
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FT DISULFID 184 198 BY SIMILARITY.
FT DISULFID 208 233 BY SIMILARITY.
FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 23 A -> AACGSDLLTKLVAENLPCVHLNPQWPSPSHCPGRG
FT WSNPLPPAA (in isoform 2).
FT /FTId=VSP_005401.
SQ SEQUENCE 260 AA; 28048 MW; EF4395B8C83E660 CRC64;
Query Match 37.7%; Score 515.5; DB 1; Length 260;
Best Local Similarity 41.4%; Pred. No. 3.6e-39;
Matches 106; Conservative 39; Mismatches 96; Indels 15; Gaps 8;
QY 4 AGNPGWFLGVLIGVAGSLVSGSCQ---IINGEDCSPHSQPQQAALVWENELFCSGVL 60
DB 8 AAKTW-MFL--LLLG--GAWAGHGRAQEDKVLGHGECQSPQQAALFGQQLCGGVL 62
QY 61 VHPQWLSAAHCFQNSYITIGLGLSLEADQBPFGQMVESASVRAHPYINRPLLA---NDL 117
DB 63 VGGNWLTAACHKPKYVRLGDHSLQKQGP-SQEIPVVGSIHPHCYNSSDVEDHNDL 121
QY 118 MLKLDSEVSDDIIRTSIASOFTAGNSCLVSGWGLLANGR--MTVLQCVNVSVSE 175
DB 122 MLLQLRDAQSLGSKVKPISLADHCTQPGQKCTVSGWGTVPSPRENFDTLNCARVKIPQ 181
QY 176 EVCSKLYDPLYPHSMFCAGGQDQKDSGSGGGLICNGYLQGLVFGKAPCQGVGPG 235
DB 182 KCCEADAYEGQITDGMVCAAGSKG-ADTCQGSQGLVCLDGLQITSGWSDPCGRSDKPG 240
QY 236 VYTNLCKFTWEIKTV 251
DB 241 VYTNICRYLDMIKKII 256
RESULT 10
ID KLKA RAT STANDARD; PRT; 244 AA.
AC P36375;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Glandular kallikrein 10 precursor (EC 3.4.21.35) (Tissue kallikrein)
DE (T-kininogenase) (K10) (Proteinase B) (Endopeptidase K) (Fragment).
GN K10 OR K10-10.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE-Kidney, and Submandibular gland;
RX MEDLINE=93041794; PubMed=1420203;
RA Ma J.-X., Chao J., Chao L.;
RT "Molecular cloning and characterization of rKlk10, a cDNA encoding T-kininogenase from rat submandibular gland and kidney."
RL Biochemistry 31:10922-10928(1992).
RN [2]
SEQUENCE OF 10-32; 95-124 AND 179-232.
RX MEDLINE=91224135; PubMed=2026164;
RA Gutman N., Elmoujahed A., Brillard M., du Sorbier B., Gauthier F.;
RT "Microheterogeneity of rat submaxillary gland kallikrein k10, a member of the kallikrein family."
RL Eur. J. Biochem. 197:425-429(1991).
RN [3]
SEQUENCE OF 10-32 AND 97-133.
RC TISSUE=Submaxillary gland;
RX MEDLINE=90153911; PubMed=2303430;
RA Xiong W., Chen L.-M., Chao J.;
RT "Purification and characterization of a kallikrein-like T-kininogenase."
RL J. Biol. Chem. 265:2822-2827(1990).
RN [4]
SEQUENCE OF 10-32 AND 97-117.
RX MEDLINE=88198057; PubMed=3482210;

Query Match 37.6%; Score 515; DB 1; Length 244;
Best Local Similarity 42.4%; Pred. No. 3.7e-39;
Matches 101; Conservative 42; Mismatches 77; Indels 18; Gaps 5;

RA Kato H., Nakanishi E., Enjyoji K., Hayaishi I., Oh-Ishi S., Iwanaga S.;
RT "Characterization of serine proteinases isolated from rat submaxillary gland: with special reference to the degradation of rat kininogens by these enzymes."
RL J. Biochem. 102:1389-1404(1987).
CC -!- FUNCTION: Glandular kallikreins cleave Met-Lys and Arg-Ser bonds in kininogen to release Lys-bradykinin. This protein may be involved in the regulation of renal function.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage of Arg-|-Xaa bonds in small molecule substrates. Highly selective action to release kallidin (lysyl-bradykinin) from kininogen involves hydrolysis of Met-|-Xaa or Leu-|-Xaa.
CC -!- SUBUNIT: Heterodimer of a light chain and heavy chain linked by a disulfide bond.
CC -!- TISSUE SPECIFICITY: Kidney and submandibular gland, where it is found in the granular convoluted tubule and striated duct cells. It is likely that the enzyme is mainly synthesized in the granular convoluted tubules and then transferred to other tissues by release into the vasculature or interstitial space.
CC -!- PTM: PROBABLY N- AND O-GLYCOSYLATED. IT HAS CARBOHYDRATE MOIETIES OF ALPHA-METHYL-D-MANNOSIDE AND N-ACETYL-D-GLUCOSAMINE GROUPS.
CC -!- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.
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CC
CC EMBL; S48142; AAB24071.1; -
CC PIR; A44284; A44284.
CC PIR; B35545; B35545.
CC HSSP; P00759; ITON.
CC MEROPS; S01.165;
CC InterPro; IPR009003; Cys_Ser_trypsin.
CC InterPro; IPR001254; Peptidase_S1.
CC InterPro; IPR001314; Peptidase_S1A.
CC Pfam; PF00089; trypsin; 1.
CC PRINTS; PR00722; TRYPTOPSYN.
CC SMART; SM00020; TRYPSIN_DOM; 1.
CC PROSITE; PS02440; TRYPSIN_DOM; 1.
CC PROSITE; PS00134; TRYPSIN_HIS; 1.
CC PROSITE; PS00135; TRYPSIN_SER; 1.
CC Hydrolase; Serine protease; Glycoprotease; Signal; Multigene family.
FT NON TER 1 1
FT SIGNAL <1 3 PROBABLE.
FT PROPEP 4 9 ACTIVATION PEPTIDE (PROBABLE).
FT CHAIN 10 244 GLANDULAR KALLIKREIN 10.
FT CHAIN 10 96 T-KININOGENASE LIGHT CHAIN.
FT CHAIN 97 244 T-KININOGENASE HEAVY CHAIN.
FT ACT_SITE 48 48 CHARGE RELAY SYSTEM.
FT ACT_SITE 103 103 CHARGE RELAY SYSTEM.
FT ACT_SITE 196 196 CHARGE RELAY SYSTEM.
FT DISULFID 15 156 BY SIMILARITY.
FT DISULFID 33 149 BY SIMILARITY.
FT DISULFID 135 202 BY SIMILARITY.
FT DISULFID 167 181 BY SIMILARITY.
FT DISULFID 192 217 BY SIMILARITY.
FT CARBOHYD 76 76 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 91 91 O-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 126 126 O-LINKED (POTENTIAL).
FT CARBOHYD 142 142 N -> IET (IN REF. 3).
FT CONFLICT 115 116 IT -> DS (IN REF. 3).
FT CONFLICT 128 128 E -> G (IN REF. 3).
FT CONFLICT 133 133 S -> G (IN REF. 3).
SQ SEQUENCE 244 AA; 27305 MW; BAB4D40547EB79C0 CRC64;

QY	29	SOIINGEDCSPHSQPWQAALVMENELFCSGVLVHPQWVLSAAHCFQNSYTTIGLGLHSLFA	98
Db	8	SRIVGKYCKEKSQPQWVAII--NEVLGCGVLDPSPWVITAAHCYNHYVHLGRNNLFE	65
QY	89	DOEPSQWVEASLSVRHPSYRNPLL-----ANDMLIKLDESVSSEDITRIS	136
Db	66	D-EPPAQYRFVFNQSPHPDY-KPFLMRNTRRGDDYSNDMLLHLSPADITDGVKVID	123
QY	137	IASQPTAGNSCLVSGWLL--ANGEMPTVLCQNVSVVSEEVCSKLYDPLVHPSWFCAG	194
Db	124	LPTEEPKVGSTCLASGWSGKPLINWELPDQLCVNIHLHSNEKCI EAYEQKVTDLMLCAG	183
QY	195	GQDQKDCSNGSGGPLICNGVYLGVLSPGKAPCGQVGPVVYTNLCCKETETIKTVQ	252
Db	184	EMDGRKDTCKGSGGPLICDGLQGITSGNVEFCAEPYNGVYTKLTKFTSWIKYWK	241

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RESULT 11
TRY3_CHICK
ID TRY3_CHICK STANDARD; PRT; 248 AA.
Q0629;
AC 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Trypsin II-P29 precursor (EC 3.4.21.4).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Pancreas;
RX MEDLINE=95251611; PubMed=7733885;
RA Wang K.; Gan L.; Lee I.; Hood L.E.;
RT "Isolation and characterization of the chicken trypsinogen gene
family.";
RT Biochem. J. 307:471-479(1995).
RL C
RL C
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: High levels are seen in the pancreas while
CC lower levels are found in the liver, spleen and thymus.
CC -!- SIMILARITY: Belongs to peptidase family S1.

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CC	CC	use by non-profit institutions as long as its content is in no way
CC	CC	modified and this statement is not removed. Usage by and for commercial
CC	CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC	CC	or send an email to license@isb-sib.ch).
CC	CC	-----
DR	DR	EMBL; UI1517; AAA73914.1; -
DR	DR	PIR; S55066; S55066.
DR	DR	KSSP; P00763; IDPO.
DR	DR	MEROPS; S01.151; -
DR	DR	InterPro; IPR009003; Cys_Ser_trypsin.
DR	DR	InterPro; IPR001254; Peptidase_S1.
DR	DR	InterPro; IPR001314; Peptidase_G1A.
DR	DR	Pfam; PF00089; trypsin; 1.
DR	DR	PRINTS; PR00722; CHYMOTRYPSIN.
DR	DR	SMART; SMO0020; Tryp_Src; 1.
DR	DR	PROSITE; PS50240; TRYPSIN_DOM; 1.
DR	DR	PROSITE; PS00134; TRYPSIN_HIS; 1.
DR	DR	PROSITE; PS00135; TRYPSIN_SER; 1.
KW	KW	Hydrolase; Serine protease; Digestion; Pancreas; Zymogen;
KW	KW	Calcium-binding; Signal; Multigene family.
FT	FT	SIGNAL 1 16 BY SIMILARITY.
FT	FT	PROPEP 17 25 ACTIVATION PEPTIDE (BY SIMILARITY).
FT	FT	CHAIN 26 248 TRYPSIN II-P29.
FT	FT	ACT_SITE 65 65 CHARGE RELAY SYSTEM (BY SIMILARITY).

FT	77	METAL	CALCIUM (BY SIMILARITY).
FT	79	METAL	CALCIUM (VIA CARBONYL OXYGEN)
FT			(BY SIMILARITY).
FT	82	METAL	CALCIUM (VIA CARBONYL OXYGEN)
FT			(BY SIMILARITY).
FT	87	METAL	CALCIUM (BY SIMILARITY).
FT	109	ACT SITE	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	202	ACT SITE	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	32	DISULFID	BY SIMILARITY.
FT	50	DISULFID	BY SIMILARITY.
FT	134	DISULFID	BY SIMILARITY.
FT	141	DISULFID	BY SIMILARITY.
FT	173	DISULFID	BY SIMILARITY.
FT	198	DISULFID	BY SIMILARITY.
FT	196	SITE	REQUIRED FOR SPECIFICITY (BY SIMILARITY).
SQ	248 AA;	SEQUENCE	248 AA; ES516B076222B588E CRC64;

RESULT 12

KLK3	MUSEE
KLK3_KLK3	KLK3
ID	ID
AC	P00757
DT	21-JUN-2006
DT	21-JUN-2006
DT	21-JUN-2006
DT	21-JUN-2006
DT	21-JUN-2006
DT	21-JUN-2006
DE	Gland
DE	mGSK
GN	KLX m
ON	Mus m
OS	Eukary
OC	Mammalia
OC	Euarchonta
OX	NCBI_
OX	[1]
RN	SEQUENCE
RP	MEDLI.
RA	Ullrich
RA	"Iesh
RT	nerv
RL	DNA 3'
RL	(2)
RP	SEQUENCE
RP	MEDLI.
RX	Evans
RA	"Gene"
RT	are c
RL	EMBO
RL	(3)
RP	SEQUENCE
RP	MEDLI.
RX	

RA Thomas K.A., Baglan N.C., Bradshaw R.A.;
RT "The amino acid sequence of the gamma-subunit of mouse submaxillary
RL gland 7 S nerve growth factor."; J. Biol. Chem. 256:9156-9166(1981).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (3.15 ANGSTROMS) OF 7S COMPLEX.
RC STRAIN=Swiss Webster; TISSUE=Submaxillary gland;
RA MEDLINE=98035451; PubMed=9351801;
RX Bax B., Blundell T.L., Murray-Rust J., McDonald N.Q.;
RT "Structure of mouse 7S NGF: a complex of nerve growth factor with
RL four binding proteins."; J. Biol. Chem. 264:1275-1285(1989).
RL Structure 5:1275-1285(1989).
CC -!- FUNCTION: 7S NGF alpha chain stabilizes the 7S complex. The beta
CC dimer promotes neurite growth. The gamma chain is an arginine-
CC specific protease; it may also have plasminogen activator
CC activity as well as mitogenic activity for chick embryo
CC fibroblasts.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage of Arg-|-Xaa bonds in
CC small molecule substrates. Highly selective action to release
CC kallidin (lysyl-bradykinin) from kininogen involves hydrolysis of
CC Met-|-Xaa or Leu-|-Xaa.
CC -!- COFACTOR: Binds 2 zinc ions per 7S complex. The zinc ions are
CC bound at the alpha-gamma interfaces.
CC -!- SUBUNIT: 7S nerve growth factor is composed of two alpha chains,
CC a beta dimer composed of identical chains, and two gamma chains.
CC -!- MISCELLANEOUS: This precursor is cleaved into segments to produce
CC the active form of the gamma chain, which occurs naturally as
CC combinations of either two or three segments held together by
CC disulfide bonds: B1 and A, or B1, C and B2.
CC -!- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X01399; CAA25645.1; -
DR EMBL; X01798; CAA25928.1; -
DR EMBL; X01799; CAA25930.1; -
DR PIR; A91005; NGMSG.
DR PDB; 1SGF; 27-MAY-98.
DR MEROPS; S01.170; -
DR MGD; MGI:97322; Ngf.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Glycoprotein; Multigene family; Zymogen;
KW Metal-binding; Zinc; Signal; Growth factor; 3D-structure.
FT SIGNAL 1 18
FT PROPEP 19 24
FT CHAIN 25 261
FT CHAIN 25 107
FT CHAIN 112 261
FT ACT_SITE 65 65
FT ACT_SITE 120 120
FT ACT_SITE 213 213
FT METAL 231 231
FT METAL 236 236
FT DISULFID 31 173
FT DISULFID 50 66
FT DISULFID 152 219
FT DISULFID 184 198
FT DISULFID 209 234
FT CARBOHYD 102 102
N-LINKED (GLCNAC. . .).

FT DOMAIN 25 107
FT DOMAIN 112 261
FT DOMAIN 112 164
FT DOMAIN 165 261
FT CONFLICT 108 111
FT STRAND 26 26
FT STRAND 29 30
FT STRAND 33 35
FT TURN 37 38
FT TURN 39 44
FT TURN 45 46
FT STRAND 47 56
FT TURN 57 58
FT STRAND 59 62
FT HELIX 64 66
FT STRAND 72 75
FT STRAND 79 79
FT TURN 80 81
FT TURN 85 86
FT TURN 88 97
FT TURN 99 100
FT HELIX 103 105
FT TURN 118 119
FT TURN 122 126
FT TURN 148 149
FT STRAND 151 156
FT STRAND 159 159
FT STRAND 167 167
FT STRAND 170 170
FT STRAND 172 179
FT HELIX 181 187
FT TURN 194 195
FT STRAND 196 200
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FT TURN 210 211
FT TURN 213 214
FT STRAND 216 219
FT TURN 220 221
FT STRAND 222 229
FT TURN 234 235
FT TURN 237 238
FT STRAND 241 245
FT HELIX 246 249
FT HELIX 250 258
FT TURN 259 259
SQ SEQUENCE 261 AA; 28998 MW; 4870748E174AF7C8 CRC64;

Query Match 37.2%; Score 509; DB 1; Length 261;
Best Local Similarity 39.5%; Pred.No. 1.4e-38;
Matches 103; Conservative 48; Mismatches 86; Indels 24; Gaps 6;
QY 10 WFL-GYLILGVAG-SLVGSCSQIINGEDCSPHSQPWQAALVMEELFCGVLVHPQWVL 67
DB 2 WFLILFALLSLGGIDAAPPVQSGRIVGFKCKNSQPHVAVYRYTQYLCGGVLLDENWYL 61
QY 68 SAACFQNSYTTGLGLHSLEADQEPGSONVEASLSVRHPEYRPL-AND 116
DB 62 TAAHCYDDNYKWLGNKNNLFKD-EPSAQHRFVSKAIPHPGFNNSLMRKHIRLEYDYSND 120
QY 117 LMLIKLDESVSBSDDTIRISIASQCPTAGNSCLVSGWGLLANGRMPTVLQ-AND 170
DB 121 LMLRLSKADITDVTKPTLTPEEPKLGSTCLASGWSIT-PTKQFTDDLXCVNL 176
QY 171 SVVSEEVCSKLYDPLVHPMFACGGQDQKQSCNGSDGGGLICNGVLOGVIFGKAPCGQ 230
DB 177 KLLPNEDCAKAIKVTDMALCAGEMDGGKDTCKGDSGGGLICDGLVLOQITTSWGTFCGE 236
QY 231 VGVPGVYTNLCKFTWIEKTV 251
DB 237 PDMFGYTKLNKFTSWIKOTM 257
RESULT 13

RESULT 14

29 SQIINGEDCSPHSQPWQAALVMENELFCSGVLVHPQWVLSAAHCFQNSYTI GLGLHSLEA 88

KW Hydrolase; Serine protease; Digestion; Pancreas; Zymogen;
KW Calcium-binding; Signal; Multigene family.
FT SIGNAL 1 15
FT PROPEP 16 24
FT CHAIN 23 247
FT ACT SITE 64 64
FT METAL 76 76
FT METAL 78 78
FT METAL 81 81
FT METAL 86 86
FT METAL 86 86
FT ACT SITE 108 108
FT ACT SITE 201 201
FT DISULFID 31 161
FT DISULFID 49 85
FT DISULFID 133 234
FT DISULFID 140 207
FT DISULFID 172 186
FT DISULFID 197 221
FT SITE 195 195
SQ SEQUENCE 247 AA; 26269 MW; D74892BA584E4A8 CRC64;
Query Match 37.0%; Score 506; DB 1; Length 247;
Best Local Similarity 40.5%; Pred. No. 2.4e-38;
Matches 100; Conservative 50; Mismatches 89; Indels 8; Gaps 6;
QY 11 FLGYLILGVAGSL-VSGSCSQTINGDCSPHQPWQAALWMENELFCSGVLVHPQWLSA 69
Db 6 FLAF--LGAVALPLDDDDKIVGGYTCQKNSLPYQVSL-NAGYHFCGSLINSQWVYSA 52
QY 70 AHCFONSYYTIGLHSLADQEPGQVSEASLSVRHPEYNRELLANDMLIKLDESVSSES 129
Db 63 AHCKSRIOVRLGEHNIDV-VEGGEQFIDAAKIIRHPSYNANTFNDIMLIKNSPATLN 121
QY 130 DTIRSIASQCPTAGNSCLVSGWG--LLANGEMPTVLOCVNVSVSEVCSKLYDELYH 187
Db 122 SRVSTVSLPRSCSGGKCLVSGWNTLSSGTNYPSLLOCLDAPVLSDSCKSSYPGKIT 181
QY 188 PSMFACAGGGQDQKSDSCNGDSGGPLICNGYLQGLVSPFGKAPCGQGVGPVYTNLCKFTWI 247
Db 182 SNMFCLGFLEGGKDSQGDGSGPVCNGQLQGVVSWGYG-CAQKGPVYTKVCNVVNI 240
QY 248 EKTQAS 254
Db 241 QQTVAAN 247

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Job time : 18 secs